Title: Perfect score:

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AX325799 Sequence
AX325800 Sequence
AX325812 Sequence
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AX325817 Sequence
AX325818 Sequence
                                                                                                                           AF110375 Aegilops
AX349066 Sequence
AF250137 Triticum
AB019624 Triticum
AX325803 Sequence
AX325804 Sequence
AX135804 Sequence
AF110374 Aegilops
X07932 Barley MRNA
X07931 Barley DNA
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                    AF474373 Hordeum v
                                               AF113843 Triticum
AB029064 Triticum
AF113844 Triticum
                  AB029061 Triticum
AB029063 Triticum
X57233 Wheat waxy
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AF110373 Triticum
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AF110375 Aegilops
                                                                                        AB029062 Triticum
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Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 1 10-JAN-2002;
Aventis CropScience GmbH (DE)
Location/Qualifiers
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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op G	1081		1140
Qy	1141	aggtgccacagactagtatttcaggcgactgggatatagccacgcctattgtttcgtg	1200
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g qq	1441		1500
Qy	1501	aggaagcaatcccgggccatgcagcgccattgccacgcccagcgaaagcgaaggcgag	1560
qq	1501	AGGAAGCATCCCGGGCCATGCAGCGCCATTGCCACGCCCAGCGAAAAGCGAAGGCGA	1560
Qy	1561	agcgagagcacacatggcccccagaactgaaagcgaggagcacacagagaaggcgcgtgc	1620
qq	1561	AGCGAGAGCACATGGCCCCCAGAACTGAAAGCGAGGGGGCACACGAGAAGGCGCGTGC	1620
δy	1621		1680
qq	1621	GCGTGGACATCACAGCAGGAACACCCACCGGCAGCCCACCGGGCGGG	1680
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Qy	1861	cgctcggcacgcacgcacgcaggcagaaacaaacaaacaa	1920
QQ	1861	CGCTCGGCACGCACGCACGCAGGCAGAACAAACAAACAAA	1920
Qy	1921	ctccactcaacgtcgcctttcaggacgatgcttcggtgccttaagacacctacct	1980
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qq	2041	ITTAAAGCACCGAAGCTGCGTCCCGCCTTTCATTACACGGGCCATGCATG	2100

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1 (sites)
Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the three Waxy genes encoding the granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Triticum aestivum gene for starch synthase (GBSSI), complete cds. AB019622.1 GI:4760579 Starch Synthase (GBSSI).
Triticum aestivum DNA.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                           Murai, J. Taira, T. and Ohta, D.

Murai, J. Taira, T. and Ohta, D.

Direct Submission

Submitted (10-NoV-1998) Jun Murai, Osaka Prefecture University,

College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531,

Japan (E-mail: junki@demeter.plant.osakafu-u.ac.jp,

Tel:81-722-54-9409, Fax:81-722-54-9409)

Location/Qualifiers

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/db_xref="taxon:4565"
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Isplation and characterization of the four Waxy genes encoding the Isplation and characterization of the four Waxy genes encoding the granule-bound starch synthase in tetraploid wheats

ppl. Biol. Sci. (1999) In press

(bases 1 to 2781)

Mural, J., Taira, T. and Ohta, D.

Direct Submission

Submitted (16-JUN-1999) Jun Mural, Osaka Prefecture University,

College of Agriculture, 1-1 Gakuen-cho, Sakai, Osaka 599-8831,

Japan (B-mail:junki@demeter.plant.osakafu-u.ac.jp,

Tel:81-722-54-9409, Fax:81-722-54-9409)
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VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMYKNCMIQDLSWK
                                                                                                                            PLN 27-JAN-2001
                                                                                                                                              Triticum turgidum subsp. dicoccoldes waxy gene for starch synthase (GBSSI), complete cds.
AB029061
                                                                                                                                                                                                                                             starch synthase (GBSSI).
Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA.
Triticum turgidum subsp. dicoccoides
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Triticum.
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                                                                                              join(13. .333,416. .496,581. .679,789. .942,1068. .1168,
258. .1621,1713. .1892,1988. .2179,2270. .2356,2455. .2583,
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VGASAAPKQSRKPHRFDRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
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/protein_id="BAA77350.1"
/db_xref="GI:4760580"
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/organism="Triticum turgidum subsp. durum"
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join[1. 321,404. 484,569. .667,777. .930,1056. .1156,
1256. .1609,1701. .1880,1976. .2167,2258. .2344,2443. .2571,
2665. .2781)
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Triticum durum waxy gene for starch synthase (GBSSI), complete cds.
AB029063
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Triticum durum DNA.
Triticum turgidum subsp. durum
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Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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                                               gaccggcggtgcctctccatggtggtgcgcgccacgggcaqcgggcgtgatgaacctcgtg 3379
gactttactgactggctggatctcgcagatcaaggtcgttgacaggtacgagagggtgag
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Isolation and characterization of th
gradule-bound starch synthase in tet.
Appl. Biol. Sci. (1999) In press
2 (bases I to 2781)
Murai, J., Taira, T. and Ohta, D.
Direct Submission
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Submitted (04-DEC-1990) J.R. Clark, WYE COLLEGE, UNIVERSITY OF
LONDON, DEPT OF BIOCHEMISTRY & BIOLOGICAL SC., NR. ASHFORD KENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3441 goctcoccgocgccatggcogtaagcttgcgccactgcctcttataaatgtttcttcct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2781;
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/protein_id="BAA88511.1"
/db_xref="G1:6624285"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%; Score 465; DB 8; Le
100.0%; Pred. No. 1.1e-245;
.ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
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bread wheat.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAWAXYSS
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/product="glycogen (starch) synthase"
/protein_id="CAA40509.1"
/db_xref="d1:J902"
/db_xref="8WISS-PROT:P27736"
/db_xref="RWISS-PROT:P27736"
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/GRABAPKOSRKPHERDRRCLEWNYRATGSGGMNLVFVGAEWAPWSKTGGLGDVLGGL
PAAMAANGHRVWVISPRYDQYKDAWDTSVISEIKVVDRYERVRYFHCYKRGVDRVFVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPCFLEKVRGKTKEKIYGPDAGTDYEDNQQRFSLLCQAALEVPRILDLNNNPHFSGPY
2 (bases 1 to 2186)
Clark,J.R., Robertson,M. and Ainsworth,C.C.
Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3159 cecagetegecacetecggeacegtecteagegteacegacagattecggegtecaggtt 3218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgccctggagcaagactggcggcctcggcgacgtcctcggggggcctccccgccgccatgg 3458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 CGAGCGCCCCCAAAGCAAACCACAAACCGCACCGATTCGACCGGCGGTGCCTCTCCA 262
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                                                                                                        Erratum:[[published erratum appears in Plant Mol Biol 1991
Oct;17(4):957]]
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                                                             encoding the waxy protein
Plant Mol. Biol. 16 (6), 1099-1101 (1991)
91322506
                                                                                                                                                                                                                    organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                      /cell_line="Chinese spring"
/tissue_type="endosperm"
/clone_lib="lambda gt10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                             /chromosome="7A, 7B, 4B"
                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="waxy"
/EC_number="2.4.1.11"
                                                                                                                                                                                                                                         /db_xref="taxon:4565"
                                                                                                                                                                         Location/Qualifiers
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/traislation="MAALVTSQLATSGTVLSVTDRFFRRGFOGLRPRNPADAALGIRT
VGASAAPKQSRKPHRGNRRCLSMVANGHRVWVISPRYDQYKDAWDTSVISETKVVDBY
BENYEFECYRRCVDRVFVDHPCFLESKYRGKFKREKISTSGPAGTDYSDONGDRFSLLCQAA
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SPYYABELISGEARGCELDNIMRLTGITGINWGMDVSEWDPTREKRFLTVNVTOYTALE
GKRAINREALQAEWGLPVDRYPLATGREEKGPDVWHAIPEIVKBEDVQIYLLG
TGKRERLLKSVSEEKFPTWYRAVVRENAPLAHQMMAGADVLAVTSRFEPCGLJOLQG
MRYGTPCAASYGGLVOTIVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVG
TPAXHEMVKNCMIQDLSWKGPAKNBEDVLLELGVESEPGIVGEEIRPLALENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 1801)
Vrinten, P.L. and Nakamura, T.
Direct Submission
Submitted (14-DEC-1998) Crop Breeding, Tohoku National Agricultural Experiment Station, Shimo-Kuriyagawa, Morioka, Iwate 020-01, Japan Location/Qualifiers
                                                                                                                                      PLN 20-APR-1999
                                                                                                                                                                                                                                                                                        Triticum aestivum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
                                                                                                                                        AF113843 1ear PLN 20-APR-199
Triticum aestivum granule-bound starch synthase precursor (Wx-Al)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Non-functional Wx-Alb allele of waxy wheat; sportaneously mutated Wx-Al gene" | 32. 1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="granule-bound starch synthase precursor"
/protein_id="AAD26155.1"
/db_xref="GI:4588607"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.1%; Score 156; DB 8; Length 1801;
100.0%; Pred. No. 3e-74;
Live 0; Mismatches 0; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                     #Golecular characterization of waxy mutations in wheat Mol. Gen. Genet. 261 (3), 463-471 (1999)
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Vinten, P., Nakamura, T. and Yamamori, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
                                                                                                                                                                                  mRNA, Wx-Alb allele, complete cds AF113843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cultivar-"Waxy"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="Wx-A1"
/note="Waxy protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             586 g
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PLN 20-APR-1999

AF113844 2028 bp mRNA linear PLN 20-APR-19 Triticum aestivum granule-bound starch synthase precursor (Wx-Dl)

mRNA, Wx-D1b allele, complete cds AF113844

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

AF113844.1 GI:4588608

Triticum aestivum

ORGANISM

bread wheat.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticae; Triticae;

2 (bases 1 to 2028) Vrinten, P.L. and Nakamura, T. Direct Submission Submitted (14-DEC-1998) Crop Breeding, Tohoku National Experiment Station, Shimo-Kuriyagawa, Morioka, Iwate 020-01, Japan

MEDLINE REFERENCE

AUTHORS JOURNAL

TITLE

JOURNAL

AUTHORS

REFERENCE

2028
 organism="Triticum aestivum" /cultivar="Waxy"

Location/Qualifiers

FEATURES

/db_xref-"taxon:4565"

/gene="Wx-D1"

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/db_xref="taxon:4567"

Join(1. .321,418. .498,590. .688,799. .952,1093. .1193,

1293. .1646,1731. .1910,1993. .2184,2265. .2351,2439. .2567,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Join(1. 321,418 . 498,590 . 688,799 . 952,1093 . 1193,
1293 . 1646,1731. . 1910,1993. . 2184,2265. . 2351,2439. . 2567,
2888. . 2804)
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TGASAAR(OSRKAHRGSRCLSMVYRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
PPAMAANGHRYWYISPRYDGYKDAMDTSVSEIKVAADEXERYRFHCKRGVDRVFVD
PPCFLEKVRGKTKEKIYGPDAGTDYEDNOLFRSLLCQAALEAPRILDINNNRPYFSGPY
EBDVWFVCNDHITGLIACXXGNYGSNGIYMTRKVAFCIHIISYQGRFSFDDFAQLNL
PDFFKSSFDFIDGYDVFRCRKINWMRAGILQADKVLTVSPYYRAELIISGRARGCELD
NIMRLTGITGIVGMDVSEWDPFKDKFLAVNYDVTTALEGRALNKELQABVGLPVDR
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VBGKTGFHMGRLSVOCNVVERADVKKVYTTRLEGRALNKEFTRSLOGLYDTI
VBGKTGFHMGRLSVOCNVVERADVKKVYTTRKRAVKVVGTPAYHGKNKNCMIQDLSWK
OFFNNREDVLLELGYBGGSEPGVIGEILAPLAMENVAAP"
                                                                                                                                            PLN 21-DEC-1999
                                                                                                                                                          Triticum durum waxy gene for starch synthase (GBSSI), complete cds.
                                                                                                                                                                                                                                                                                                                                                                                        1 (sites)
Mural,J., Taira,T. and Ohta,D.
Mural,J., Taira,T. and Ohta,D.
Scolation and characterization of the four Waxy genes encoding the granule-bound scir. (1999) In press
2 (bases 1 to 2804)
                                                                                                                                                                                                                                                                                 Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mutal, ..., ..., Direct Submission
Submitted (16-JUN-1999) Jun Mural, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-cho, Sakal, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, Tel:81-22-54-9409, Fax:81-722-54-9409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Triticum turgidum subsp. durum"
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                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="starch synthase (GBSSI)"
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100.0%; Pred. No. 2.7e-39;
tive 0; Mismatches 0;
121 GAGGCCCCGGAACCCGGCGGATGCGGCGCTCGGCAT 156
                                                                                                                                          DNA
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/db_xref="G1:6624287"
                                                                                                                                    2804 bp
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                                                                                                                                                                                                                                   Starch synthase (GBSSI).
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                                                                                                                                                                                                        AB029064.1 GI:6624286
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VERSION
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JOURNAL
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AB029064
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GEDVVEVCNDWHTGLLACYLKSNYQSNGIYRAKVAFCITHNISYQGRESFDDFAQLNL
BYBFKSSEDFIOGYDREVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELD
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KVPLVAFIGKLEEQVGEPVMATA IPEILKEEDVQIVLLGTGKKKFFRLLKSIERKFPS
KVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLGGGMRYGTPACAGASTGGLVUTI
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF163319 2127 bp mRNA linear PLN 14-FEB-2000 Triticum aestivum granule-bound starch synthase I (Wx-DI) mRNA, Wx-DIa allele, complete cds.
                                                                                                                                                                                                                                                                                      3111 gctgcaggtagccacacctgcgcgcgccatggcggctctggtcacgtcccagctcgcca 3170
                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                           Score 77; DB 8; Length 2028; Pred. No. 2e-30; 0; Mismatches 0; Indels
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100.0%; Pred. No. 200.00; Mismatches
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                                                                                                                                    628 g
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                                                                                                                                    614 c
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Gaps ; 0

0; Indels

93; Conservative

Matches

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Local Similarity

3322 ccggcggtgcctctccatggtggtgcgcgcacgggcagcggcggcatgaacctcgtgtt 3381

AF113844

RESULT

/translation="MAALVTSQLATSGTVLGITDRFRRAGFGGVRPRSPADAALGMRT VGASAAPTQSRKAHRGTRRCLSMVVRATGSGGMNLVFYGAEMAWSKYGGLGDVLGGL PPAMAANGHRYMVISPRYDQYKDAWDTSVVSEIKVVDKYERVRYFHCYKRGVDRVFVD HPCFLEKVRGKTKEKIYGPDAGTDYEDNQORFSLLCQAALEVPRILNLDNNPYFSGPY

/product="granule-bound starch synthase precursor" /protein_id="AAD26156.1" /db_xref="GI:4588609"

/note="Waxy protein; non functional" /codon_start=1

/gene="Wx-D1"

CDS

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                                        granule-bound starch synthase in tetraploid wheats Appl. Biol. Sci. (1999) In press 2 (bases 1 to 2793)
Murai,J., Taira,T. and Ohta,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP"
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/protein_id="BAA88510.1"
/db_xref="GI:6624283"
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                                              Pooideae, Triticeae, Triticum.
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Triticum aestivum DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  starch synthase (GBSSI).
Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA.
Triticum turgidum subsp. dicoccoides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="maalutsolatsgrulgitdrprpragegogvrprspadalgmrt
vgasaaptgsrkahrgtrrclsmvvratgsggmnlvfvgarmapmsktgglgdvlggl
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HPCFLERYRGKTKRIYTGPBAGTDPDNQDRPSLLCQAALEVPRILNLDNNPYFSGPV
GEDVVFVCNDWHTGLLACYLKSNYQSNGITRAAKVAFCIHNISYGGRFSFDDFAQLN
PDRFKSSFDFTDGYDRYVBGRKINWMRAGILQADKVLTVSPYTAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDJITTALEGKALMKEALQAEVGLPVDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVRAVVRENAPLAHQMMAGADVLAVTSREEPCGLIQLQGMRYGTPCACASTGGLVDT I
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSWK
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                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (28-JUN-1999) Crop Breeding, Tohoku National Agricultural
Experiment Station, Akihira 4, Morioka, Iwate 020-0198, Japan
                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                          wheat granule-bound starch synthase I and II are encoded by separate genes that are expressed in different tissues plant physiol. 122 (1), 255-264 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="granule-bound starch synthase I"
/protein_id="AAR34135.1"
/db_xref="GI:6969978"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.0%; Score 77; DB 8;
100.0%; Pred. No. 2e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Triticum aestivum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar-"Chinese Spring"
/db_xref="taxon:4565"
/chromosome="7D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="immature seed"
                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                      2 (bases 1 to 2127)
Vrinten, P.L. and Nakamura, T.
                                                                                                                                           1 (bases 1 to 2127)
Vrinten, P.L. and Nakamura, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /allele="Wx-DIa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Wx-DI"
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Matches 77; Conservative
                                                               Triticum aestivum
                                              bread wheat.
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join(1. .324,424. .504,593. .691,805. .958,1092. .1192,
1262. .1615,1708. .1887,1974. .2165,2249. .2335,2433. .2561,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(1. .324,424. .504,593. .691,805. .958,1092. .1192.
[262. .1615,1708. .1887,1974. .2165,2249. .2335,2433. .2561,
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YGEDVYFVCNDRFTGLLACYLKSNYQSSGIYRTAKVAFCIHNISYQGRFSFDDFAQLN
LPDRFKSSFDFIDGYDKPVEGRKINNMKAGILQADKVLTVSPYYAEELISGEARGCEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNINRLTGITGIVNGMDVSEMDPAKDKFLAANYDVITALEGKALNKEALQAEVGLPVD
RKVPLVARFGRLEEQKGPDVMIAAIPEILKEEDVQIVLLGIGKKKFERLLKSVEEKFP
SKVRAVVRENAFLAHQMMAGADVLAVISRFEPCGLIQLQGMRYGTPCACASTGGLVDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="maalvtsolatsgtvlgitdrfrragfoggvrprspadplgmrt
tgasaapkqosrkahrgtrrclsmvvratgsagmilvfvgaemapwsktgglgdylgg
lppamaanghrymvisprydovkdamdtsvvseikvadevervrfhcykrgvdrvfv
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the four Waxy genes encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO19623 2818 bp DNA linear PLN 05-AUG-19
Triticum aestivum gene for starch synthase (GBSSI), complete cds.
AB019623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3538 tgcaggccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggacg 3597
                                                                                                                                                                                                                                                                Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, college of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, rel:81-722-54-9409, Fax:81-722-54-9409)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="mriticum turgidum subsp. dicoccoides"
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/ LTGBS 1 ALLO = "NALUYEQLATSGTVLG ITDRFRRAGFOGVRPRSPADAPLGMRT
/ LTGBS 1 ALLO = "NALUYEQLATSGTVLG ITDRFRRAGFOGVRPRSPADAPLGMRT
GASAPKOGNRAHGTRRCLSMYVRATGSAGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRWYL SPRYDOYKDAWDTSVVBSIKVADADS FRORYETHOYKROVDRYPV
DHPCFLEKVNGKTKEKI TORPAGTDYEDNOLRFSLLCOAALBAPRILDLINNNPYFSGP
VGEDVVFVCNDWHTGLACYLKSNYOSSG IYRTAKVAFCIHNISYQGRFSFDDFAQLN
LPPRFKSSFDFIDGYDVFVCNTNWKRGAILQADKTLVSPYYSAELISGSARGCEL
DNINRLTGITG IYNGMDYSEMDPRADKFLAANYDYTTALEGSALNKENLOAFGCEL
DNINRLTGITG IYNGMDYSEMDPRADKFLAANYDYTTALEGSALNKENLOAFGCEL
SKYPLVAFIGRLEEQKGPDVMIAAIPELLKESDVQIVLLGTGKKKFFRLLKSVEEKFP
SKVRAVVRNAPLAGMMAGADVLATYSRFEBCGLIOLQGMRYGTPCAASTGGLVDT
IMBGKTGFHAGRLSYDCNVVPEPADVKKVYTTLKRANKVUGTPAYHEMVKNCMIQDLSW
KGPAKNWEDVLLEGGVEGSEPGYLGEBIAPLAMENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                Join(13. .336,436. .516,605. .703,817. .970,1104. .1204,
1274. .1627,1720. .1899,1986. .2177,2262. .2348,2446. .2574,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(13. .336,436. .516,605. .703,817. .970,1104. .1204,
[274. .1627,1720. .1899,1986. .2177,2262. .2348,2446. .2574,
Mrai,J., Taira,T. and Ohta,D.
Solation and characterization of the three Waxy genes encoding the
granule-bound starch synthase in hexaploid wheat
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Triticum monococcum granule-bound starch synthase WX-TmA protein
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
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                                                                                                                                                                                                     Submitted (10-NOV-1998) Jun Murai, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junkiedemeter.plant.osakafu-u.ac.jp, Pel:81-722-54-9409; Fax:81-722-54-9409)
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100.0%; Pred. No. 2.1e-30;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="starch synthase (GBSSI)"
/protein_id="BAA77351.1"
/db_xref="GI:4760582"
                                                                                                                                                                                                                                                                                                                                     1. .2818
/organism="Triticum aestivum"
/db_xref="taxon:4565"
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                                                                                                                                                        Murai, J., Taira, T. and Ohta, D. Direct Submission
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                                                                                Gene 234 (1), 71-79 (1999)
99321800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="waxy
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/organism="Triticum monococcum"
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/db_xref="traxon:4568"
join(<32. .355,444 .524,613. .711,830. .983,1127. .1227,
1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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RKVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSYEEKFP
SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDT
IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAXHEMVKNCMIQDLSW
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VGASAAPKQOSRKAHRGTRRCLSVVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIKVADEYERVRYFHCFKRGVDRVFV
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Genome (1999) In press 2 (bases 1 to 2834)
Zan.L., Bhave,M., Fairclough,R., Konic,C., Rahman,S. and Appels,R. Direct Submission
Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
Location/Qualifiers
1. 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear PLN 30-OCT-2000 starch synthase I (GbssI) gene,
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1 (bases 1 to 2289)
McCue, K.F., Hurkman, W.J., Tanaka, C.K. and Anderson, O.D. Starch Branching Enzymes Sbel and Sbe2 from Wheat (Triticum aestivum cv. Cheyenne): Molecular Characterization, Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'granule-bound starch synthase WX-TmA protein"
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834 c 831 g 591 t
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Pred. No. 2.1e-30;
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tive 0; Mismatches
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/db_xref="G1:6318538"
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/gene="wx-TmA"
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/db_xref="taxon:32630"
/note="Oligonucleotide"
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1 (bases 1 to 2893)
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Yan, L., Bhave, M., Fairclough, R., Konic, C., Rahman, S. and Appels, R.
                                                                                                                 Submitted (11-JUL-2000) United States Department of Agriculture, Agricultural Research Service, 800 Buchanan Street, Albany, CA
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/note="glucosyltransferase; ADP glucose glucosyl
    Expression, and Homolog Assignment by Diffferential PCR
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Best Local Similarity 100.0%; Pred. No. 1.2e-2
Matches 72; Conservative 0; Mismatches
                                                                                                                                                                                                                              /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                        /tissue_type="endosperm"
204. .2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                      transferase; waxy; Wx"
                                                                                                                                                                                                                                                 /cultivar="Cheyenne"
/db_xref="taxon:4565"
                                                                                                                                                                             Location/Qualifiers
1. .2289
                              Unpublished
2 (bases 1 to 2289)
McCue, K.F. and Anderson, O.D.
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204. .2021
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Aegilops tauschii
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                                                                              AUTHORS
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1370. .1723,1809. .1988,2071. .2262,2347. .2433,2532. .2660,
2777. .>2893)
/gene="wx.TtD"
                                                                                                                                                                                                                                                         join(32. 352,443. 523,620. 718,823. 976,1128. 1228,
1370. 1723,1809. 1988,2071. 2262,2347. 2433,2532. 2660,
2777. 2893)
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Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                               /product="granule-bound starch synthase WX-TtD protein"
/protein_id="AAF06938.1"
/db_xref="G1:6318542"
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Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 4 10-7AN-2002;
Aventis CropScience GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2893;
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100.0%; Pred. No. 5.7e-2
Live 0; Mismatches
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                                                                                         /organism="Aegilops tauschii"
/cultivar="CPI 110799"
/db_xref="taxon:37682"
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20 c 15 a BASE COUNT ORIGIN

0; Gaps Query Match 1.8%; Score 68; DB 6; Length 72; Best Local Similarity 100.0%; Pred. No. 1.6e-25; Matches 68; Conservative 0; Mismatches 0; Indels

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Search completed: July 31, 2002, 16:11:39 Job time: 14356 sec

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Sequence 4, Appli
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                                      Compugen Ltd.
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US-08-742-185-101
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US-08-960-038-23
US-09-350-0253-5
US-08-574-959A-8
US-09-357-014-6
US-08-374-959A-6
US-08-374-959A-6
US-08-574-959A-6
US-08-574-959A-6
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Gapop 60.0 , Gapext 60.0
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Sequence 19 Sequence 10 Sequence 11 Sequence 21 Sequence 22 Sequence 23 Sequence 23 Sequence 23 Sequence 23 Sequence 23 Sequence 24 Sequence 11 Sequence 12 Sequence 12 Sequence 12 Sequence 12 Sequence 13 Sequence 13 Sequence 13 Sequence 15	
2. 0.6 58 4 US-09-580-923-9 2. 0.6 58 4 US-09-580-923-10 2. 0.6 66 3 US-08-984-511-16 2. 0.6 66 3 US-08-984-511-17 2. 0.6 66 4 US-09-860-038-20 2. 0.6 66 4 US-09-580-923-20 2. 0.6 66 4 US-09-580-923-20 2. 0.6 66 4 US-09-580-923-21 2. 0.6 188 1 US-08-466-670-21 2. 0.6 188 2 US-08-291-011-1 2. 0.6 188 4 US-09-266-065-1 2. 0.6 188 4 US-09-26-065-1 2. 0.6 656 4 US-09-390-774A-1 2. 0.6 550 4 US-09-390-774A-1 2. 0.6 678 4 US-09-378-781 2. 0.6 678 4 US-09-378-781 2. 0.6 678 4 US-09-378-781	ALIGNMENTS Hequence 25, Application US/08679645 actent No. 6350934 GENERAL INFORMATION: APPLICANT: Edington, Brent E. APPLICANT: Edington, Brent E. APPLICANT: McSwiggen, James A. ADDRESSEE: Lyon & Lyon CITY: Los Angeles STREET: Soulte 4700 COMPUTION NUMBER: 12, 1996 ATTORNEY-CAGNY UNDERS: 21, 2994 ATTORNEY-CAGNY UNDERS: 21, 2994 ATTORNEY-CAGNY UNDERS: 21, 2994 ATTORNEY-CAGN
20000000000000000000000000000000000000	RESULT 1 US-08-679-645-; Sequence 25, Sequence 26, BAPLICANT APPLICANT APPLI
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US-08-623-906A-1/c
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..2144, 2226..2289, 2413..2513, 2651..2760, 2858
..3101, 3212..3394, 3490..3681, 3793..3879, 3977
..4105, 4227..4343)
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100.0%; Pred. No. 6.9e-09;
                                                                                                                                                                   Ouery Match 1.0%; Score 39; DB 4; Length 2267; Best Local Similarity 100.0%; Pred. No. 6.8e-09; Matches 39; Conservative 0; Mismatches 0; Indels
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APPLICATION NUMBER: US/08/941,445A FILING DATE: 30-SEP-1997 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,855 FILING DATE: 30-SEP-1996 ATTORNEY AGENT INFORMATION:
NAME: Winner, Ellen P
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: S7370 Manhattan Circle
CITY: Boulder
                                                                                                                                                                                                                                                       3576 egetaegaceagtaeaaggaegeetgggaeaceagegte 3614
                                                                                                                                                                                                                                                                               Sequence 4, Application US/08941445A Patent No. 6107060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (303) 499-8080 TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 H: 4800 base pairs
nucleic acid
DEDNESS: double
OGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                         LENGTH: 2267 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COOLOGY: linear
US-08-679-645-25
                 SEOUENCE CHARACTERISTICS:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-941-445A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                      08-941-445A-4
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Gaps
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102
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100.0%; Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Milltia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-0CT-1996
Query Match
Best Local Similarity 100.0%; Pred. No. 4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 38989 GAAGAAGAAGAAGAAGAAGAAGAAGAAG 39019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WH194-07A2 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-UUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08623906A Patent No. 5874217 GENERALINFORMATION:
APPLICANT: Stevenson, Tamara
                                                                                                                                                  Sequence 101, Application US/08742185; Patent No. 6020476; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 861-9540 INFORMATION FOR SEQ ID NO: 101:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: DNA (genomic) US-08-742-185-101
                                                                                                                                                                                                                                                       APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DALE: A GR
NUMBER OF SEQUENCES: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 43795 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  APPLICANT: Page, David C. APPLICANT: Reijo, Renee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 30-OCT-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Massachusetts
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LOCATION: 1..28
OTHER INFORMATION: /note= "Nucleotides 1-28 are unique
OTHER INFORMATION: flanking sequence"
APPLICANT: Dvorak, Jan
APPLICANT: Halverson, Joy
TITLE OF INVENTION: Microsatellite Sequences for Canine
TITLE OF INVENTION: Genotyping
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.7%; Score 25; DB 2; Length 252; Best Local Similarity 100.0%; Pred. No. 0.03; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                        ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 104..252
OTHER INFORMATION: /note= "Nucleotides 104-252 are
OTHER INFORMATION: unique flanking sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 29.103
OTHER INFORMATION: /note= "Nucleotides 29-103 are
OTHER INFORMATION: repeat sequence"
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DARA: APPLICATION NUMBER: US/08/623,906A FILIG DATE: CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanping
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J.
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: 36,677
REFERENCE/TO INFORMATION:
TELEPHONE: 415-781-1989
TELEPHONE: 415-398-3249
                                                                                                                                                                                                                                                  ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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US
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US-08-941-445A-6
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Gaps
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APPLICANT: SCHERMAN, Daniel
APPLICANT: WILS, PIETRE
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
TITLE OF INVENTION: WITH AN IMMOBILIZED OLIGONUCLEOTIDE
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match

0.7%; Score 25; DB 3; Length 2542;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/941,445A
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                       PILICALIUM MOLES
FILING DATE: 30-SEP-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Winner, Ellen P
REGISTRATION NUMBER: 28,547
REFERENCE/DOCKET NUMBER: 89-97
TELECOMMUNICATION INFORMATION:
TELEPROME: 3033,499-8080
TELEPRAX: 3033,499-8080
TELEPRAX: 3033,499-8080
TELEPRAX: 2349-8080
TELEPRAX: 2343 D NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 2542 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08860038
Patent No. 6287762
GENERAL INFORMATION:
5370 Manhattan Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 2542 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453..2282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CE HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                    80303
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US-08-941-445A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-860-038-23
                                                             COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 24; DB 4; Length 1865; 100.0%; Pred. No. 0.09; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/574,959A
FILLIG DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                       GENERAL INFORMATION:
APPLICANT Allen, Stephen M.
APPLICANT: Sakai, Hajime
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Amino Acid Transporters
FILE REPERENCE: BB-1200
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/370,253
CURRENT FILING DATE: 1999-08-09
EARLIER APPLICATION NUMBER: 60/097,222
EARLIER FILING DATE: August 20, 1998
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: LAHIVE & COCKFIELD 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: DFN-008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AGGAAGAAGAAGAAGAAGAAG 27
                                                                      US-09-370-253-5/c; Sequence 5, Application US/09370253; Patent No. 6165792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3211 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Oryza sativa
US-09-370-253-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02109-1875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
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                                                          RESULT
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APPLICANT: Scherman, Daniel
APPLICANT: Scherman, Daniel
APPLICANT: Mils, Pierre
APPLICANT: Cameron, Beatrice
APPLICANT: Blanche, Francis
TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELIX FORMATION WITH AN TITLE OF INVENTION: IMMOBILIZED OLIGONUCLEOTIDE
FILE REFERENCE: 03804,0138-01
CURRENT APPLICATION NUMBER: US/09/580,923
CURRENT FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 08/860,038
PRIOR APPLICATION NUMBER: 09/860,038
PRIOR APPLICATION NUMBER: 09/860,038
PRIOR PILING DATE: 1997-06-09
PRIOR PILING DATE: 1997-06-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 24; DB 4; Length 39;
100.0%; Pred. No. 0.089;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: 01190nucleotide US-09-580-923-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; Fred. No. 0.ur
Matches 24; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
                                                                                                                                                                                                                        ATTORNIA AGENT LINCOMATION:
NAME: SAVIZEKY ESQ., MATTIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST94090-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
TERE: nucleic acid
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                      APPLICATION NUMBER: WO FR95/01468
FILING DATE: 08-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oy 2377 aggaagaagaagaagaagaagaag 2400
APPLICATION NUMBER: US/08/860,038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2377 aggaagaagaagaagaagaag 2400
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/15162
FILING DATE: 16-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 23, Application US/09580923
; Patent No. 6319672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AGGAAGAAGAAGAAGAAGAAGAAG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                   PRIOR APPLICATION DATA:
                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-860-038-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi and Jack L. Strominger TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                             Query Match

O.6%; Score 24; DB 2; Length 3211;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION NUMBER: 08/574,959
FILING DATE: CURNOWND-
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISCHERNI NUMBER: 36.07
REGISCHERNI NUMBER: 36.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 24; DB 4; Length 3211;
100.0%; Pred. No. 0.09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: DEN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COCATION: 439..3157
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-357-014-8
                                                                                                                                                                                                                                   2377 aggaagaagaagaagaag 2400
                                                                                                                                                                                                                                                                          2423 AGGAAGAAGAAGAAGAAGAAG 2446
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                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09357014 Patent No. 6291645 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3211 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0
Watches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CDNA
                                                               439..3157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
MOLECULE TYPE: CDNA
                                      ; NAME/KEY;
; LOCATION:
US-08-574-959A-8
                                                                                                                                                                                                                                                                                                                                                                US-09-357-014-8
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and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
                                                                                 GENERAL INFORMATION:
APPLICANT: Jaekyoon Shin, Insil Joung, Ratna K. Vadlamudi
APPLICANT: and Jack L. Strominger
TITLE OF INVENTION: p62 POLYPEPTIDES, RELATED POLYPEPTIDES
TITLE OF INVENTION: 22
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

O.6%; Score 24; DB 2; Length 3901;
Best Local Similarity 100.0%; Pred. No. 0.091;
Matches 24; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/574,959A
FILING DATE: 19-DEC-95
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: DFN-008
TELEPHONE: (617)227-7400
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3113 AGGAAGAAGAAGAAGAAGAAG 3136
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                                            Sequence 6, Application US/08574959A
Patent No. 5962224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/09357014
; Patent No. 6291645
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS TOCATION: 439..3847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                            STREET: 60 Sta
CITY: Boston
STATE: Massach
RESULT 11
US-08-574-959A-6
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INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.'
Matches 23; Conservative
                                                                                                                                                                                                                                                                        polyA_signal
4607..4612
                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
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EDNESS: single
                                                                                                                                                                                                               TATA_signal 2275..2281
                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                       CAAT_signal 2234..2243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94304
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                                                                                                                                                       NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                          ; LOCATION:
US-08-688-376-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH:
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                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                       FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
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TITLE OF INVENTION: NOVEL PROCESS FOR PRODUCING SUBSTANCES
TITLE OF INVENTION: IN MAMMARY GLAND OF TRANSGENIC ANIMAL BY USING MC26 GENE
TITLE OF INVENTION: EXPRESSION-REGULATORY REGION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/357,014
FILING DATE: 19-Jul-1999
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/688,376 FILING DATE: 30.UL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DILWORTH & BARRESE 4350 LaJolla Village Drive, Suite 300
                                                                                                                                                                                                                                                        REPERENCE/DOCKET NUMBER: DEN-008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-5440
TELEPHONE: (617)227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 3901 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; SEQUENCE DESCRIPTION: 439.3847
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-357-014-6
                                                                                                                                                           APPLICATION NUMBER: 08/574,959
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
WIDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Pepper, Frederick W.
REGISTRATION NUMBER: 31, 286
REFERENCE/DOCKET NUMBER: 567-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-688-376-1; Sequence 1, Application US/08688376; Patent No. 6018039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
TELEFAX: 619-453-2839
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            San Diego
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92122
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100.0%; Pred. No. 0.27;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 24; DB 3; Length 5394;
100.0%; Pred. No. 0.091;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ), ORGANISM: Chimeric tomato spotted wilt virus S RNA US-08-553-619B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,619B
FILING DATE: December 1, 1995
CLASSIFICATION: 800
CLASSIFICATION: ROWATION:
NAME: Marcus "Wyner, Lynn
REGISTRATION NUMBER: 34,869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUDRESSEE: No. 5919705artis Crop Protection STREET: 975 California Avenue CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: DeHaan, Petrus T.
TITLE OF INVENTION: Virus Resistant Plants
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                          2377 aggaagaagaagaagaagaag 2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08553619B Patent No. 5919705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 137-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/354-1125
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2621 base pairs
5394 base pairs
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GENERAL INCORNATION:
APPLICANT: Ecker, Joseph R. et al.
TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene
TITLE OF INVENTION: and Pathogens
NUMBER OF SEQUENCES: 82
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5650553ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatchtIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,822A
FILING DATE: IJ-JUN-1994
CLASSTFICATION NUMBER: 34,293
TACRNEY/AGENT INFORMATION:
TELEFHOME: REATCHI, LOTI Y.
REGISTRATION NUMBER: 34,293
TELECOMMUNICATION INFORMATION:
TELEFHONE: (215) 568-3100
TELEFRAM: (215) 568-3499
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TELETTH: 3387 base pairs
TYPE: nucleic acid
STRANDEDRESS: single
                                                                                                                        RESULT 15
US-08-261-822A-5/c
; Sequence 5, Application US/08261822A
; Patent No. 5650553
                            389 ttttttattttttatttt4 411
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Gaps ö Query Match

O.6%; Score 23; DB 1; Length 3387;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 23; Conservative 0; Mismatches 0; Indels

2377 aggaagaagaagaagaagaa 2399

Search completed: July 31, 2002, 16:14:02 Job time: 13649 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic . nucleic search, using sw model

July 31, 2002, 10:43:18; Search time 2776.96 Seconds (Without alignments) 18396.367 Million cell updates/sec Run on:

US-09-899-718A-1 3785 Perfect score:

1 gittggtttcgctgtttttc......tggaccgcgtgttcgtcgac 3785 Sequence:

OLIGO_NUC Gapop 60.0 , Gapext 60.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

Word size :

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

em_gss_inv:* em_gss_pln:* em_gss_vrt:* gb_gss:* em_gss_hum:* em_esthum:*
em_esthum:*
em_estin:*
em_estov:*
em_estpl:*
em_estpl:*
em_htc:*
gb_est1:* gb_est2:* gb_htc:* EST:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	יַ שִּׁלַתְ ַלַּלָּךְ ַ ַ מַ	BE3/3417 601225078
SUMMARIES	AW44831 AL506396 AL506396 BE602243 AL508959 AL508163 BE402419 BE414303 BE414303 A2113646 A2113646 A21364811 BM368238 A2462781 AZ368386 AZ368386	71101000
DB	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1
% Query Match Length DB	527 513 513 513 513 513 513 513 513	1
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Score	322 522 522 522 522 522 522 522 523 77 76 77 837 77	
Result No.	C C C C C C C C C C C C C C C C C C C	

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ALIGNMENTS

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EST 03-JAN-2001 mRNA sequence.	acheopl ae; Poc			Gaps
EST	ı; Tr			
527 bp mRNA linear BRY Triticum aestivum cDNA clone P56-1P, 1 G1:12019366	bread wheat. Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooideae ; Triticae: mrificum	1 (bases 1 to 52) Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm Oupublished (2000)	C.S.T.RO. C.S.T.RO. GPO Box 1600, Canberra, ACT, Australia Tel: 61 2 6246 5054 Fax: 61 2 6246 5000 Email: bryanc@pi.csiro.au. Location/Qualifiers // Crganism="Triticum aestivum" // Chyanism="Triticum aestivum" // Chyanism="Triticum aestivum"	/clone="P56-lp" /clone_lib="BRY" /cell_type="endosperm" 115 a 176 c 163 g 73 t 8.5%; Score 322; DB 9; Length 527; llarity 100.0%; Pred. No. 3.7e-141; Conservative 0; Mismatches 0; Indels
AW448831 BRY_1580 BJ AW448831 AW448831.1 EST.	<pre>bread wheat. Triticum aes Eukaryota; V Spermatophyt ; Triticeae:</pre>	(base larke, B enes ac npublis	C.S.I.R.O. GPO BOX 166 GPO BOX 166 Fax: 61 2 0 Fax: 61	115 a similari si Cons
31 TION TION N OS	SOURCE DO ORGANISM TO ES	REFERENCE 1 AUTHORS C. TITLE GG JOURNAL UG COMMENT C.	CC CG GG TC F2 F2 F3 F3 F3 F3 F3 F3 F3 F3 F3 F3 F3 F3 F3	BASE COUNT 115 a ORIGIN Query Match Best Local Similarity Matches 322; Conserv

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HVSMEh0098D06f Hordeum vulgare 5-45 DAP spike BST llbrary
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0098D06f,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                AL508933 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY10D16V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 513)
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.
Est sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W
Contact: Michalek W
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
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/lab_host="XLOLR"
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                                                1.4%; Score 52; DB 9; Length 513;
100.0%; Pred. No. 3.3e-13;
tive 0; Mismatches 0; Indels
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/organism="Hordeum vulgare"
        0; Mismatches
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/db_xref="taxon:4513"
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SOURCE
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Hordeum VULGARE CIONE HY02P18T 5', MRNA SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institute for plant Genetics and Crop Plant Research Corrensstr.3, D-06466 Gatersleben, Germany Email: michalekelipk-gatersleben.de, http://pgrc.ipk-gatersleben.de seq primer: T3 primer for 5'end.
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/lab_host="XLOLR"
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ORGANISM

ACCESSION

AL506396

RESULT

VERSION KEYWORDS

TITLE AUTHORS

COMMENT

FEATURES

REFERENCE

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ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

EST 04-JAN-2001

linear

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/ncce="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhOI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhOI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp.

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AL506567 Hordeum vulgare CDNA clone HY03121T 5', mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Michalek W
Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
Location/Qualifiers
                               AL508959 Hordeum vulgare Barke developing caryopsis (3.-15.DAP) Hordeum vulgare cDNA clone HY10E20V 5', mRNA sequence.
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//tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
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Michalek W., Weschke, W., Pleissner, K.-P. and Graner, A.
The sequencing and analysis in barley
Unpublished (2000)
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      mRNA
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/cultivar="Barke"
/db_xref="taxon:4513"
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(bases 1 to 700)
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//ADD. LUDSE - SOLIKE.
//ADD. LUDSE - SOLIKE.
//ADD. RIVERSIDE (FERTION, SJC1058). Whole Callifornia, Riverside (Fenton, SJC1058). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, poly(A) RNA was purfiled from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give phluescript SK(-) cDNA phagamids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson University genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, YU, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                         Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Y., Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Close, S.J., Oates, R. and Maih, D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On Ang 21, 2000 this sequence version replaced gi:9859804.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University Genomics Institute
                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Iriticeae; Hordeum.

    Chases 1 to 558)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0098D06f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total hq bases = 215
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 550.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
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Hordeum vulgare
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Query Match

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Query Match 1.3%; Score 51; DB 10; Length 579; Best Local Similarity 100.0%; Pred. No. 9.7e-13; Matches 51; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
                                                                                                                                                                               213 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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245 c 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Triticeae; Triticum.
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Hordeum vulgare
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contains less than two ambiguities. The maximum length was
                                                                                                                                                                                                                                                                                                                            /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: Xhol; manA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seg primer: T3 primer for 5'end.
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                       Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
                                                                                                                                                                                                                             /clone_lib="Hordeum vulgare Barke developing caryopsis
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/lab_host="XLOLR"
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Corrensstr.3, D-06466 Gatersleben, Germany
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                                                                                                                          /organism="Hordeum vulgare"
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                                               Seq primer: T3 primer for 5'end.
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                                                                                                                                               /cultivar="Barke'
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(3'-end of CDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is I kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE402419 579 bp mRNA linear EST 21-JUL-2000 CSB007G05F990908 ITEC CSB Wheat Endosperm Library Triticum aestivum cDNA clone CSB007G05, mRNA sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 1.4%; Score 52; DB 9; Length 700; Best Local Similarity 100.0%; Pred. No. 3.2e-13; Matches 52; Conservative 0; Mismatches 0; Indels
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Email: bryanc@pi.csiro.au.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                       Seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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ORIGIN
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AUTHORS
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COMMENT
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Contact: Holton T
Centre for Plant Conservation Genetics, Southern Cross University Po Box 157, Lismore NSW 2480 AUSTRALIA
Fax: 61 2 6622 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AZ113646 421 bp DNA linear GSS 12-MAY-2000 RPCI-23-447D2,TJ RPCI-23 Mus musculus genomic clone RPCI-23-447D2,
                                                                                                                                       EST 24-JUL-2000
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,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 421)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                     BE414303 639 bp mRNA linear EST 24-JU SCU008.C04.R990714 ITEC SCU Wheat Endosperm Library Triticum aestivum cDNA clone SCU008.C04, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.3%; Score 51; DB 10; Length 639;
100.0%; Pred. No. 9.6e-13;
tive 0; Mismatches 0; Indels
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/note="Vector: Bluescript II SK(-)"
215 c 201 g 86 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tholton@sou.edu.au
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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                                                                                                                                                                                                                    BE414303.1 GI:9412135
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bread wheat.
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and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)
Other GSSS: RPCI-23-447D2.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0200
Fax: John Center Dr., Rockville, MD 20850, USA
Tel: and Centre Dr., Rockville, MD 20850, USA
Clones are derived from the mouse BAC library RPCI-23. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://Pacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (inf@dessen.com). BAC
Http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
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1 (bases I to 494)
1 (bases I to 494)
Genes active in developing wheat endosperm
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoR1; Site_2: EcoR1; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoR1 and EcoR1 Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoR1 sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

1 134 c. 24 g 248 t.
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100.0%; Pred. No. 2.1e-09,
tive 0; Mismatches 0;
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Tel: 61 2 6246 5054
Fax: 61 2 6246 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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Division of Plant Industry
C.S.I.R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="C57BL/6J
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AZ733073 165 bp DNA linear GSS 25-JAN-2001
RPCI-24-118F9.TV RPCI-24 Mus musculus genomic clone RPCI-24-118F9,
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/note="Vector: pTaRBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTaRBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejongemail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end page: http://www.thori.org/bacpac/orderingframe.htm). BAC end page: http://www.tigr.org/fdb/bac_ends/mouse/bac_end_intro.html Plate: 118 row: F column: 9
                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 165)
Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer.K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                            Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Burinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BamH1 sites using Mbol partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A2462781 260 bp DNA linear GSS 04-0CT-200
1M0271G17F Mouse 10kb plasmid UGG1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse BAC End Sequences from Library RPCI-24 Unpublished (1999)
Other_GSSs: RPCI-24-118F9.TJ
244 GCGTCACCGACAGATTCCGGCGTCCAGGTTTTCAGGGCCT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.0%; Score 37; DB 12; I 100.0%; Pred. No. 5.3e-06; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Eukaryotic Genomics
The Institute for Genomic Research
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/clone="RPCI-24-118F9"
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                                                                                                                                                                                                                                       AZ733073.1 GI:12496755
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AZ462781.1 GI:10620906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 C
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                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BM368238 444 bp mRNA linear EST 10-JAN-200 EBed01_SQ002_J02_R IGF Barley EBed01 library Hordeum vulgare cDNA clone EBed01_SQ002_J02 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Triticeae; Hordeum.

1 (bases 1 to 444)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
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0
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All sequence has a Phred quality score of 20 or over
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.1%; Score 40; DB 10; Length 444;
                                                                                                                                                                                                                                                                Length 494;
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/clone_lib-"IGF Barley EBed01 library"
/tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                    3189 gcgtcaccgacagattccggcgtccaggttttcagggcct 3228
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
                                                                                                                                                                                                                                                           Score 41; DB 9; L
Pred. No. 5.5e-08;
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                      /organism="Triticum aestivum"
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Unit of Genomics
Scottish Crop Research Institute
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                                                                                                                                   /cell_type="endosperm"
170 c 160 a
                                                                /db_xref="taxon:4565"
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                                                                                                                                                            160 g
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                                                                                                               /clone_lib="BRY"
                                          /cultivar="Wyuna"
                                                                                           /clone="P51-2A"
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Matches 41; Conservative
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GSS 04-OCT-2000

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house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 [pb]ARL29072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 260)
Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
Musculus C57BL/G1 (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                              Mouse whole genome scaffolding with paired end reads from 10\mathrm{kb} plasmid inserts
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/clone="UUGCIM0271G17"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
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100.0%; Pred. No. 4.9e-06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plate: 0271 row: G column: 17
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: plasmid ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 т. .260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 37; Conserva
                             Mus musculus
  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
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                        ORGANISM
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ORIGIN
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                                                                                                       REFERENCE
                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRSION
                                                                                                                                                                                                                                                                                                                COMMENT
SOURCE
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polymerase act of the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114 ybplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moublished (2000)
Contract: Robert B. Weiss
Contract: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentla; Sclurognathi; Murinae; Musinae; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/note="Vector: PWD42rv; Purified genomic DNA from M.
musculus C57BL/G1(male) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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1.0%; Score 37; DB 12; I
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 37; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2379 gaagaagaagaagaagaagaagaagaagaagaag 2415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0118 row: M column: 19
Seg primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .380 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Class: plasmid ends
High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0118M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: July 31, 2002, 14:54:43
Job time: 15085 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
Fax: 801 585 7177
Mus musculus
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 14:02:43; Search time 389.91 Seconds Run on:

(without alignments) 16666.721 Million cell updates/sec

US-09-899-718A-1 Perfect score: Title:

1 gtttggtttcgctgttttc.....tggaccgcgtgttcgtcgac 3785 Sequence:

Scoring table:

OLIGO_NUC Gapop 60.0 , Gapext 60.0

1736436 seqs, 858457221 residues

Word size :

Searched:

3472872 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* N_Geneseq_032802:*

/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1989.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1990.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1991.DAT:* | SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1981.par: *
| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1981.bar: *
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| SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/Na1988.bar: * | SIDS1/gcgdata/hold-geneseg/geneseqn-embl/NA1992.DAT:* | SIDS1/gcgdata/hold-geneseg/geneseqn-embl/NA1993.DAT:* | SIDS1/gcgdata/hold-geneseg/geneseqn-embl/NA1994.DAT:*

/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1997.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:*/SIDS1/geneseqn-embl/NA2001B.DAT:*/SIDS /SIDS1/gcgdata/hold-geneseq/geneseqn-emb//NA1995.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:* 14: 15: 16: 17: 19:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT

	Description	ACTEGO VGGO GEMIN	DNA COMICCIONE A F TE	Or seducing the	ger Transfer Star	zea mays waxy gene	Human toetal liver	Probe #13741 for q	Human bone marrow	Probe #13097 for a	DNA encoding novel
		AAC74569	AAX60319	AAX63355	AAV29752	35095E4	0070000	ABA352/5	AAK42405	AAI23164	AAS71148
g	3 !	21	19	18	19	22	1 (77	77	77	73
Length	6	333	1915	2267	4800	276	200	0 1 4	9/7	9/7	460
% Query ye Match Lenαth ne r		1.0	1.0	1.0	1.0	1.0			9.0		٠.
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			DNA encoding novel	2	•-	. מ		_	,	Circod Ling	encoding	encoding	encodin	encoding	encoding	done in t	ຄໍ	grandı	Chall	tuopsis tha	ontaining		icrosate	Canine genomic mic		- >		#3829 1	hone marr	#3881	Tope that	s chair	s thall	מ מ		Arce Staron syntha DNA encoding novel
e e	AASSUBS	AAS7546	ς,	_	_	_	1 AAC5215	_	<u></u>	<u>~</u>	~	3 AAS6811	3 AAS6954	3 AAS7070	e	21 AAC52482		AAC4417		A TO COLK	A D C 1 2 0 A		AAA3162	-	AAX1780	AAF139		22 ABA25363			AAC4		31 AAC36166		AA04	23 AAS86699
			11/																		140									a	~	220	949	265	286	
1.0	•	•	•	•	•	•	•										0.7				0.7	•			•			•	٠	0.7	•	•	•		0.7	
37	, ,	27	T C	31	29	29	29	29	28	27	27	27	27	27	27	56	26	26	26	26	25	25	9 6	7 10	0 10	0.7	270	25	25	25	25	25	25	25	25	25
10	12	13	7 -	* + +	15	16	17	18	19	20	21	22	23	24	25	56	c 27	28	29	30	31	m) (, ,	0 0	9 (n (7) (וויי	m .		41	c 42	4	44	45

ALIGNMENTS

AAC74569 standard; cDNA; 333 BP, RESULT AAC74569

Human ORFX ORF124 polynucleotide sequence SEQ ID NO:247. (first entry)

08-FEB-2001

Whuman; open reading frame; ORFX; detection; cytostatic; hepatotropic; wulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; antibronvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coaquilant; vasotropic; antidiabetic; whypotensive; dermatological; immunosuppressive; antiinflammatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; wantianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; ALDS; condiovascular disease; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autolmmune disorder; asthma; allergy; aplastic anaemia; noctural haemoglobinuria; burn; wound; thrombosis; contraceptive; ss.

Homo sapiens.

WO200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US08621.

98WO-US06660.

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03-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                         AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; sequences have activities such as: cytostatic; hepatotropic; vulnerary; osteopathic; antiporvulsant; antiarthritic; immunosuppressant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressant; cantidiabetic; hypotensive; dermatological; antinhological antiphematic; antithneamatory; antibacterial; antiviral; antiphematic; antithneamatory; antibacterial; antiviral; antiphematic; antithneamatory; antibacterial; antiviral; antiphematic; coagulant; vasotropic; antithneamatory; and antianaemic. The sequences can be used for determining antithyroid; and antianaemic. The sequences can be used to express ORFX proteins in gene therapy.

Complete acids can be used to express ORFX proteins in gene therapy or corp. The proteins and nucleic acids may be used to treat cancers, corp. The proteins and nucleic acids may be used to treat cancers, corp. In proteins of second anticosymmunical antibutis, cholesterol ester storage, systemic lupus corp. Thematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-glycogen-like polysaccharide production; fermentation; waxy gene; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis; non-starch branching gene; amylopectin; amylose; plant-like starch; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 1.0%; Score 39; DB 21; Length 333; Local Similarity 100.0%; Pred. No. 3.3e-08; hes 39; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 333 BP; 78 A; 96 C; 100 G; 59 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence of the maize waxy gene.
                                                                                                                                                                                                                                                                                                                                                    claim 5; Page 560; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX60319 standard; DNA; 1915 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                 31-MAR-1999; 99US-0127607.
02-APR-1999; 99US-0127636.
05-APR-1999; 99US-0127728.
30-MAR-2000; 2000US-0540763.
                                                                                                                                                                              Shimkets RA, Leach M;
                                                                                                                                       (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                   WPI; 2000-602362/57.
                                                                                                                                                                                                                                          P-PSDB; AAB40360
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The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maize; corn; Zea mays; delta-9 desaturase; GBSS; target; substrate; granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme; modulation; gene expression; transgenic plant; cleavage; canola plant; caffeine synthesis; coffee plant; nicotine production; tobacco; fruit ripening; flower pigmentation; lignin production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
1.0%; Score 39; DB 19; Length 1915;
Best Local Similarity 100.0%; Pred. No. 3.3e-08;
Matches 39; Conservative 0; Mismatches 0, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McSwiggen JA,
Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3576 cgctacgaccagtacaaggacgcctgggacaccagcgtc 3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 egetacegeceaglacaaggacectgggacaceagegte 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Granule bound starch synthase encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cuo L,
Young SA,
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 49; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX63355 standard; cDNA; 2267 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US11689.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (RIBO-) RIBOZYME PHARM INC.
                                                            (EXSE-) EXSEED GENETICS LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Folkerts O,
Skokut TA, Yo
97US-0042939
                                                                                                                                                                                                                                                                                                                                                               engineered properties
                                                                                                                        Guan H, Keeling PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOWC ) DOWELANCO.
                                                                                                                                                                                 WPI; 1998-568285/48.
                                                                                                                                                                                                                   P-PSDB; AAY16604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edington BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9710328-A2
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   04-APR-1997;
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                                                                          The present invention describes an enzymatic nucleic acid molecule (I) with RNA cleaving activity, which modulates the expression of a plant gene. Also described is a gene comprising a CDNA sequence encoding maize Delta-9 desarturase. (I) can be used to modulate expression of a gene preferably Delta-9 desarturase or a granule bound starch synthase (GBSS) gene, in a plant (preferably a maize or canola plant). (I) can be used to modulate caffeine synthesis in a coffee plant, nicotine production in a tobacco plant, fruit ripening processes in an apple, tomato, pear, chrysenthemum or marigold plant or lignin production in a rose, petunia, aspen, poplar or pine plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/note= "GC stretch, potential regulatory factor binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "GC stretch, potential regulatory factor binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= f
'note= "GC stretch, potential regulatory factor binding'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= g
/note= "GC stretch, potential regulatory factor binding'
                                                                                                                                                                                                                                  Gaps
                         Ribozyme which modulates plant gene expression - preferably modulates expression of DELTA-9 desaturase or granule bound starch synthase in maize or canola
                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                Length 2267;
                                                                                                                                                                                                           1.0%; Score 39; DB 18; Length 22, 100.0%; Pred. No. 3.3e-08; tive 0; Mismatches 0; Indels
                                                                                                                                                                                 Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;
                                                                                                                                                                                                                                             SER; starch-encapsulating region; fusion vector;
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/note= "direct repeat 1"
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/note= "direct repeat 1"
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/note= "direct repeat 1"
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/note= "direct repeat 1"
                                                            Example 9; Page 31-33; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
283..287
                                                                                                                                                                                                                                                                                                         AAV29752 standard; DNA; 4800 BP.
                                                                                                                                                                                                         Query Match 1.0%
Best Local Similarity 100.0
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                            11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                          glucosyl transferase; ss.
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         WPI; 1997-202224/18.
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AAV29752
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'note = "GC stretch, potential regulatory factor"
            /*tag= i
/note= "target duplication site (Ac7)"
                                                                                                                   /*tag= m
/note= "transcriptional start site"
1449..4343
                                                                                                                                                           /product= glucosyl transferase
/note= "contains introns"
901.,1080
                                                                                                                                                                                                                                                                                                   /number= 2
1685..1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= z
/number= 6
                                                              /*tag= k
887..900
/*tag= 1
                                                                                                                                                                                                                1081..1219
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/*tag= bb
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/*tag= cc
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/number= 9
                                                                                                                                                                                                                                              1220..1553
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/number= 6
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                                            /*tag= j
367..873
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/number= 9
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 821..828
                                 821..828
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misc_feature
                                                                         misc_feature
                                                                                                        misc_feature
                                CAAT_signal
                                                     TATA_signal
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Length 4800;

us-09-899-718a-1.oli.rng

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The sequence is that of the waxy gene which codes for glucosyl transferase. It can be used in the production of a hybrid polypeptide comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e.g. hormones, growth factors, antibodies, enzymes, dyes, immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hybrid polypeptide comprising starch-encapsulating region and protein - useful for, e.g. producing protein(s) resistant to degradation by stomach acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4800 BP; 935 A; 1414 C; 1446 G; 1005 T; 0 other;
                                                                                                       /*tag= kk
/note= "target duplication site (Spm 18)"
                   /*tag= hh
/note= "target duplication site (Ac9)"
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13
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                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0026855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EXSE-) EXSEED GENETICS LLC.
                                                                                                                                                                                                          /number= 12
3977..4105
                                                                                                                                                                                                                                       /number= 13
                                                                                                                                                                                                                                                                                                 /number= 14
4570..4575
                                                                                                                                                                             /number= 12
3880..3976
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/number= 10
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                                                                                                                                                /number= 11
3793..3879
                                                                                       'number= 11
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                                                                  ..3681
                                                                                                                            .3792
                                                                                                                                                                      /*tag= mm
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                                      .3489
                                                                                               3570..3572
         3358..3489
                                                 /*tag= ii
                                                                                                                                                                                                                                                                     /number=
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4597..46
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4593..45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guan H, Keeling P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW56484
                                                                                                                                                                                                                                                                                                                                                                              WO9814601-A1
                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1997;
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           misc_feature
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                                                                                                                                                                                                                                                                                Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
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Probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pott_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; SEQ ID NO 16571; 639pp + sequence listing; English.
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100.0%; Pred. No. 3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                      Human foetal liver single exon nucleic acid probe #16571.
                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
                                                                        3576 cyctacyaccaytacaagyacycctyyyacaccaycytc 3614
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1.0%; Score 39; DB 19; 1
100.0%; Pred. No. 3.3e-08;
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               100.0%; Pred. No. 3.3 tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanzel DK, Chen W,
                                                                                                                                                                    ABA68266 standard; DNA; 276 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000; 2000US-0180312.
26-MAY-2000; 2000US-0207456.
30-UN-2000; 2000US-0608408.
AUG-2000; 2000US-05356.
21-SEP-2000; 200US-0234687.
27-SEP-2000; 200US-023559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                             30-JAN-2001; 2001WO-US00669
                                                                                                                                                                                                                                 01-FEB-2002 (first entry)
                                 39; Conservative
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Best Local Similarity
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      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                      WO200157277-A2.
                                                                                                                                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penn SG,
                                                                                                                                                                                                   ABA68266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                          ABA68266/c
                                     Matches
                                                                                                                                            RESULT
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ABA35275 standard; DNA; 276 BP

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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #13097 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid
Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO: 16962; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.0%; Score 37; DB 22; Le
Pred. No. 36-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2379 gaagaagaagaagaagaagaagcagaagaagaagaag 2415
                                                                                                                                                                                                                                                                                                                                                                                  analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GAAGAAGAAGAAGAAGAAGCAGAAGAAGAAGAAG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                          Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI23164 standard; DNA; 276 BP
                                                                                                                                                                                                                                                                             (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                       2000US-0207456.
2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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                                                                                                                                 30-JAN-2001; 2001WO-US00668.
                                                                                                                                                              2000US-0180312
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Matches 37; Conservative
                                                                                                                                                                                                                                                                                                         Hanzel DK,
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488900/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cervical cancer; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200157278-A2
                                                                       WO200157276-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human;
                                            Homo sapiens.
                                                                                                                                                                                                      03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                          26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                              04 - FEB-2000;
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                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                          Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAI23164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single exon nucleic acid probes for analyzing gene expression in human
                                                                       Probe #13741 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                   gene expression; heart; microarray; vascular system; probe; vascular disease; hypertension; cardiac arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human bone marrow expressed single exon probe SEQ ID NO: 16962.
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Pred. No. 3e-07;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
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100.0%; Pred. No. 3e-(
+:ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                           Chen W,
                                                                                                                                                                                                                                                                                                                      2000US-0632366.
2000US-0234687.
2000US-0236359.
                                                                                                                                 congenital heart disease; ss.
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2000US-0608408
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                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease.
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Best Local Similarity 100.
Matches 37; Conservative
                                                                                                                cardiovascular disease;
                                                                                                                                                                                                                                                                                                                                                                                                                           Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488899/53
                                                                                                                                                                                        WO200157274-A2.
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27-SEP-2000;
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               ABA35275;
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                                                                                                                                                                                        (SENP). The present sequence is one such probe. The SENPS are derived from human HeLa cells. The SENPS can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                          Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                    analyzing gene expression in human cervical epithelial cells
                                                                                                                                                                                                                                                                                                                                          1.0%; Score 37; DB 22; Length 276;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                          Sequence 276 BP; 23 A; 81 C; 20 G; 152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #6952.
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                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. NO. 35.
                                                                                                                                                          Claim 25; SEQ ID No 13097; 487pp; English.
                                                                            Penn SG, Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS71148 standard; cDNA; 460 BP.
                                                      (MOLE-) MOLECULAR DYNAMICS INC.
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                                04-OCT-2000; 2000GB-0024263.
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23-AUG-2000; 2000US-0649167.
2000US-0632366.
          2000US-0234687.
2000US-0236359.
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                                                                                                 WPI; 2001-488901/53.
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03-AUG-2000;
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on bNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                           The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 460 BP; 209 A; 51 C; 128 G; 72 T; 0 other;
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Claim 1; SEQ ID No 6952; 103pp; English.
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Claim 1; SEQ ID No 26501; 103pp; English.

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in reating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                              and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPPO
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000; 2000US-0649167.
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P-PSDB; ABG26510.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oldgenes, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and advanced to the contract of the polypeptide and polymeration of mutations are among the contract of the con
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in the polynucleotide and polynucleotide sequences have applications in the polynucleotide sequences have applications in the polynucleotide and polynucleotide sequences have applications in the polynucleotide sequences have applications and the polynucleotide sequences have applications and the polynucleotide sequences have applicated and polynucleotide sequences hav
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The condition of consequence tags for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and and applied and polymers. Assessing the sequence of human and as a manufacture of the consisting and to produce other types of data and products dependent on DNA and and applied and produce other types of data and products dependent on DNA and and applied and produce other types of data and products dependent on DNA and and applied and produce other types of data and products dependent on DNA and and applied and produce other types of data and products dependent on DNA and and applied and produce other types of data and products dependent on DNA and and applied and produce other types of data and produce of new produce of the produce of the produce other types of data and produce of the produce of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid, useful for diagnosis and treatment of reduced sperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAZ gene; chromosome Yq; male infertility; sperm count; diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.8%; Score 31; DB 23; Length 711;
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Best Local Similarity
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present in interval 6D and/or 6E of the distal portion of Yq, mutations in which are associated with reduced sperm count. The DAZH gene family, including DAZH is expressed in germ cells. DAZ and DAZH nucleotide sequences may be used as a source of primers and probes for the diagnosis of reduced sperm count associated with alteration or deletion of the DAZ genes They are also used as human chromosome Y markers. Functional DAZ genes can be used in gene therapy for treating reduced sperm counts. Sequence AAZ92499 represents human DAZ CDNA, and sequences AAZ92581-292584 are genomic DAZ sequences. Sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 62490.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 90US-0161992.
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GenCore version 4.5

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2002, 12:26:27; Search time 165.21 Seconds

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26.762 Million cell updates/sec

Title: US-09-899-718A-8

Perfect score: 18 tactctggtcatgttaa 18

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Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066
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Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 1, Appli	~	Sequence 40, Appl		204,	204,	~	12,	'n	Sequence 1, Appli	Sequence 1, Appli	Ļ	~.	Sequence 91, Appl	83,	1713	Sequence 1713, Ap		Sequence 48, Appl	Sequence 1, Appli	71,	, A	Sequence 13, Appl
SUMMARIES	qı	US-08-741-411-4	US-08-602-713-11	US-08-989-493-11	US-08-147-592A-1	US-08-292-694A-1	US-08-476-062A-40	PCT-US96-01314-40	5424399-1	US-08-991-789A-204	US-09-062-451-204	US-09-457-046B-15	US-09-153-804-12	US-08-480-662-1	US-08-918-190-1	US-09-234-232-1	PCT-US96-09927-1	US-09-018-787-2		w	US-08-373-124A-1713	US-08-435-628-1713	US-08-307-499-48	US-09-299-268-48	US-08-798-000-1	US-09-475-316A-71	US-09-011-745-5	US-08-258-420-13
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Sequence 1, Appli Sequence 14, Appl Sequence 1, Appli	Sequence 14, Appl Sequence 6, Appli	5, 7	Sequence 168, App Sequence 168, App	168, 1, Ap	Sequence 3, Appli Sequence 3, Appli	Sequence 1, Appli Sequence 3, Appli	Sequence 3, Appli Sequence 3, Appli
US-08-307-499-1 US-08-307-499-14 US-09-299-268-1	US-09-299-268-14 US-08-680-327-6	US-08-756-849-5. 5278286-1	US-08-184-009-168	US-08-460-736-168 US-08-771-110-1	US-08-625-377-3 US-09-204-841-3	US-09-242-095-1 US-08-149-093A-3	US-08-911-245-3 US-08-553-058C-3
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14176 14176 14176	14176	132	601	601 736	1095	1251	1452 1452
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74.4 74.4 74.4	73	73	73	73	73	73	73
13.4	13.4	13.2	13.2	133.5	13.2	13.2	13.2
28 30 30	32	35 35	36	86	40	42	44
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ALIGNMENTS

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ADDRESSEE: INCYTE PHARMACEUTICALS, INC. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: US
                                                                                             APPLICANT: Bandman, Olga
APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL RAB PROTEINS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF-0139 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/741,411
                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/741,
RESULT 1
US-08-741-4/c
Sequence 4, Application US/08741411
Patent No. 6124116
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 890 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 415-855-055
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herewith
                                                                                                                                                                                                                                                                                                                                         Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA
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LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                94304
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US-08-741-411-4
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Query Match
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                                  Gaps
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                                ó
                                                                                                                                                                                                                                                                                   APPLICANT: Hunser, Hans-Peter; Knapp Stefan; Brust, Stefan;
APPLICANT: Griler, Lutz G.; Eberle, Josef; Kaptue, Lazare;
APPLICANT: Zekeng, L opold Achengui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
NUMBER OF EXQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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APPLICANT: Hauser, Hans-Peter; Knapp Stefan; Brust, Stefan;
APPLICANT: G rtler, Lutz G.; Eberle, Josef; Kaptue, Lazare;
APPLICANT: Zekeng, L opold Achengui
TITLE OF INVENTION: Retrovirus From The HIV Group And Its Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 80.0%; Score 14.4; DB 1; Length 1070; Best Local Similarity 93.8%; Pred. No. 48;
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                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
93.8%; Preu. ....
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APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRIARY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/602,713
FILING DATE: 16-FEBRUARY-1996
CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Hanson, No. 5798205man D. REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                    Sequence 11, Application US/08602713 Patent No. 5798205 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/08989493
; Patent No. 6162631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: LEI TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30,946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1070 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 ATACTCTTGTCATGTT 418
                                                                                                                 282 ATACTCGGGTCATGTT 267
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                           15; Conservative
                                                                       1 atactctggtcatgtt 16
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New York
         Best Local Similarity
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Gaps
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                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Opioid Receptor Genes, TITLE OF INVENTION: Compositions and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LEDER 203
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,713
FILING DATE: 16-FEBRUARY-1996
APPLICATION NUMBER: DE 195 05 262
FILING DATE: 16-FEBRUARY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/989,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson, No. 6162631man D.
TITLE OF INVENTION: (MVP-2901/94)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/08147592A
; Patent No. 6096513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                               ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
US-08-989-493-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1070 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                       PC-DOS
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APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 ATACTCTTGTCATGTT 418
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                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 atactctggtcatgtt 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Arnold, Whi
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                     NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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                                                                                                        New York City
New York
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                               IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                 COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                             10022
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                                                                                                                                                       COUNTRY:
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APPLICATION NUMBER: 07/212,573
FILING DATE: 28-JUN-1988
ATJORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00786/068003
APPLICATION NUMBER: 08/147,592
FILING DATE: 5 No. 6319686ember 1993
CLASSIFICATION: 435
                   20 May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-JUN-1990
APPLICATION NUMBER: 07/212 572
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-08-476-062A-40/c
Sequence 40, Application US/08476062A
Patent No. 5877275
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.0%
Best Local Similarity 93.8%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                        nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
LOCATION: 186..1325
                                                       APPLICATION NUMBER:
FILING DATE: 20 May
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                linear
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ZIP: 02110-2804
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Patent No. 6319686
GENERAL INFORMATION:
APPLICANT: BELL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUNA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.0%; Score 14.4; D 93.8%; Pred. No. 50; Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/292,694A
FILING DATE: August 19, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
     APPLICATION NUMBER: US/08/147,592A FILING DATE: 05-NOV-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Arnold, White & Durkee P. O. Box 4433
                                                                                                                                                                                                                    NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                           PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPICATION: 435
CLASSIPICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIPICATION: 435
                                                                                                                                                                                                                                                                                                                                  TELEX: N/A
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415 ATTCTCTGGTCATGTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 93.8
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 186..1325
US-08-147-592A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA
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STATE: Texas
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US-08-292-694A-1
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Gaps
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TITLE OF INVENTION: CONTROLLING CELLULAR IMMUNE/INFLAMMATORY
TITLE OF INVENTION: RESPONSES WITH BETAZ INTEGRINS
TITLE OF INVENTION: RESPONSES: AND ADDRESSE: ADDRESSE: ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%; Score 14.4; DB 4; Length 1410; 93.8%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: SYSTEM: Windows95
OPFWARE: FastESD for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,062A
FILING DATE: 07-JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/216,081
FILING DATE: 21-MAR-1994
APPLICATION NUMBER: 07/537,830
FILING DATE: 04-JAN-1991
FILING DATE: 07-JAN-1991
APPLICATION NUMBER: 07/539,842
ATTORNEY AGENT INFORMATION:
NAME: MARK B. WILSON
RECISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELEPHONE: (512) 418-3000
TELEPHONE: (513) 789-2679
TELERA: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
SEGURENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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APPLICANT: ARNAOUT, M. AMIN
TITLE OF INVENTION: HUMAN CR3a/b HETERODIMERS
NUMBER OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/78,871
FILLING DATE: 16-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Potter, Jane E. R. REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 204, Application US/08991789A; Patent No. 6225054; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 248 base pairs
                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 539,842
FILLING DATE: 18-JUN-1990
APPLICATION NUMBER: 22,573
FILLING DATE: 28-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 204:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                              1258 ACTCTGGTCATGTTGA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 93.8 Matches 15; Conservative
                         3 actctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 actctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQ ID NO:1:
; LENGTH: 3533
                                                                                                                                                                    ;Patent No. 5424399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-991-789A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                               5424399-1/c
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0
                                                                                                                                                                                                                                                                                                                                               80.0%; Score 14.4; DB 2; Length 3533; 93.8%; Pred. No. 56; tive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.0%; Score 14.4; DB 5; Length 3533; 93.8%; Pred. No. 56; tive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCT-0596-01314-40/c

Sequence 40, Application PC/TUS9601314

GENERAL INPORATION:
APPLICANT: M. Amin Arnaout

ITILE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN

TITLE OF INVENTION: ANTAGONISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS/2 MOGEL 502 OF 55X
OPERATION SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WORDPETFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/01314
FILING DATE: 30-JAN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-JAN-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          00786/267001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: John W. Freeman
REGISTRATION NUMBER: 29,066
                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 20154
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 3533 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 75...3530
                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                          Query Match 80.03
Best Local Similarity 93.83
Matches 15, Conservative
                 : 617/542-507
617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.89
Matches 15; Conservative
                                                                                                                                    nucleic acid
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EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Massachusetts
                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                               linear
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                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Boston
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                                                                                                                                                                                                                                                                                 US-08-476-062A-40
                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US96-01314-40
                                    TELEFAX:
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Gaps
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                                                   ;
0
80.0%; Score 14.4; DB 6; Length 3533; 93.8%; Pred. No. 56; 1; Indels 0;
                                                                                                                                                                                                                                                                                                             APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: 620 Newport
CITY: Newport Beach
STATE: CA
COUNTRY: USA
FILE REFERENCE: 53679
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SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-153-804-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                    TYPE: DNA
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APPLICANT: Croteau, Rodney et al.
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Red Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.7%; Score 13.8; DB 4; Length 248; 88.2%; Pred. No. 83; tive 0; Mismatches 2; Indels
                                                                                                  DB 4; Length 248;
                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/062,451 FILING DATE: 04-APR-1997
                                                                                                  Score 13.8; DB Pred. No. 83; 0; Mismatches
                    SEQUENCE DESCRIPTION: SEQ ID NO: 204: US-08-991-789A-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 210121.419C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09457046B Patent No. 6287835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                           Sequence 204, Application US/09062451
Patent No. 6344550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 204
                                                                                                    76.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 248 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 88.23
Matches 15; Conservative
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                                                                                                                                                                              1 atactctggtcatgtta 17
            TOPOLOGY: linear
                                                                                                      Query Match 76.73
Best Local Similarity 88.23
Matches 15; Conservative
                                                                                                                                                                                                                  71 ATGCTCTGATCATGTTA 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
US-09-062-451-204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Wach:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 0. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-09-457-046B-15
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APPLICANT: Julian Gordon
APPLICANT: Steven C. Hodges
APPLICANT: Steven C. Hodges
APPLICANT: Michael R. Klass
APPLICANT: Michael R. Klass
APPLICANT: Eite Russell
APPLICANT: Stephen D. Stroupe
TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the Urin
TITLE OF INVENTION: Tract
TITLE REPRENCE: 6180.05.01
CURRENT APPLICATION NUMBER: US/09/153,804
CURRENT FILING DATE: 1998-09-15
NUMBER OF SEQ. ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pastan, Ira APPLICANT: Pastan, ulrich APPLICANT: Brinkmann, ulrich TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN (CSP) AND AN NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                DB 4; Length 908;
                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Knobbe, Martens, Olson and Bear
620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                Score 13.8; DB
Pred. No. 99;
0; Mismatches
CURRENT APPLICATION NUMBER: US/09/457,046B CURRENT FILING DATE: 1999-12-07 NUMBER OF SEQ ID NOS: 74 SECTIVARE: PatentIn Ver. 2.1 SECTION 015 LENGTH: 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08480662
Patent No. 5759782
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/09153804
; Patent No. 6207380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Patricia Billing-Medel
                                                                                                                                                                                                                                                                     76.7%;
88.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 1336 ttctctggttatgttaa 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Maurice Cohen
APPLICANT: Paula N. Friedman
                                                                                                                                                                                                                                                                                                                                                                                           2 tactctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7
Best Local Similarity 88.2
Matches 15; Conservative
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 88.2°
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                               1 atactctggtcatgtta 17
                                                                                                                                                                          ; ORGANISM: Taxus cuspidata
US-09-457-046B-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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REFERENCE/DOCKET NUMBER: NIH112.001A TELECOMMUNICATION INFORMATION: TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,232
FILING DATE: 20-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION: <Unknown>
APPLICATION NUMBER: 08/918,190
          NAME: Israelsen, Ned A
RECISTRATION NUMBER: 29,655
REFENCE/DOCKET NUMBER: NIH112.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/09234232
; Patent No. 6232086
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 3180 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 619-235-0176
                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 1336 TTCTCTGGTTATGTTAA 1352
                                                                                                                                                                                                LENGTH: 3180 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tactctggtcatgttaa 18
                                                                                                TELEPHONE: 619-235-855
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: CA
                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                            ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-918-190-1
                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 15
US-09-234-232-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.7%; Score 13.8; DB 1; Length 3180; 88.2%; Pred. No. 1.2e+02; Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GEMERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Brinkmann, Ulrich
APPLICANT: BLINKmann, Ulrich
TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY
TITLE OF INVENTION: PROTEIN (CSP) AND ANTISENSE CSP
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
                                             COMPUTER: ADD. SYSTEM: DOS SOFTWARE: FASTSEQ VERSION 1.5 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/480,662 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: NIH112.001A
TELECOMONIACATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/918,190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/480,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESD Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08918190
Patent No. 6072031
                                                                                                                                                                                                                                                                                          29,655
                                      COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3180 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 1336 TTCTCTGGTTATGTTAA 1352
                                                                                                                                                                                                                                                                   NAME: Israelsen, Ned A
REGISTRATION NUMBER: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 76.7%
Best Local Similarity 88.2%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 tactctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                              CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE:

ORIGINAL SOURCE:
US-08-480-662-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-918-190-1
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0;
76.7%; Score 13.8; DB 3; Length 3180; 88.2%; Pred. No. 1.2e+02; tive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                            APPLICANT: Pastan, Ira
APPLICANT: Pastan, Ira
Brinkmann, Ulrich
TITLE OF INVENTION: CELLULAR APOPTOSIS SUSCEPTIBILITY
PROTEIN (CSP) AND ANTISENSE CSP
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson and Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
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TOPOLOGY: linear

HYPOTHERICAL: NO

HYPOTHERICAL: NO

PRAGMENT TYPE: CUNNown>

CRIGINAL SOURCE:

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-234-232-1

Query Match

Query Match

Atches 15; Conservative 0; Mismatches 2; Indels 0; Gaps

Qy 2 tactctggtcatgttaa 18

Db 1336 TTCTCTGGTTATGTTAA 1352

Search completed: July 31, 2002, 12:26:28

JOBA 1301 Sec
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	8		
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July 31, 2002, 12:12:12; Search time 5855.71 Seconds (without alignments) 41.489 Million cell updates/sec 27472414 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY_NUC Gapop 10.0 , Gapext 1.0 1 atactctggtcatgttaa 18 US-09-899-718A-8 18 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 EST:* Perfect score: Scoring table: Database : Searched: Sequence: Run on: Title:

em_estba:*
em_esthum:*
em_estin:*
em_estin:*
em_estov:*
em_estp!:*
em_estp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	BG531376 602559625	BF516695 NXSI_002_		AQ621441 HS_3019_B	AZ144687 SP_0041_B	BG318023 NXPV_008_	AZ207084 SP_0127_A	AQ150695 HS_3203_A	AW812504 CM4-ST018	AL212759 Tetraodon	BI287040 UI-R-CT0s	BE142340 CM3-HT014	BB024447 BB024447	BB289468 BB289468		BE556305 sq01a05.y	BE650684 UI-M-BH3-
	ID	BG531376	BF516695	BG318395	AQ621441	AZ144687	BG318023	AZ207084	AQ150695	AW812504	CNS02T50	BI287040	BE142340	BB024447	BB289468	BF147142	BE556305	BE650684
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	Query Match Length DB	1441	344	513	558	564	571	724	404	635	1026	213	225	297	303	337	350	393
*	Query Match	94.4	91.1	91.1	91.1	91.1	91.1	91.1	88.9	88.9	86.7	85.6	85.6	85.6	85.6	85.6	85.6	85.6
	Score	17	16.4	16.4	16.4	16.4	16.4	16.4	16	16	15.6	15.4	15.4	15.4	15.4	15.4	15.4	15.4
	ult No.	-	17	m	4	Ŋ	9	7	· œ	σ	10	2	12	ď	17	15	9	11
	Result No.	ا ا)		C)		c)	Č	, c) C)		Ç	J		

AQ442997 HS_5132_B AA102952 mc09d01.r BF256005 HVSMEf000 B1326958 AR071D101 AA738969 gb16h09.y AA15297 mc48c03.r	A1493734 q212g07.x AW230662 uo66d09.y AQ477545 CITBI-E1- H16901 ym39b02.rl	C84686 C84686 Dict AQ596806 HS_5206_A B1784821 Saf93999. AZ444415 1M0242014 B1784991 Saf93d11.	4	AQ016921 C17-HSP-Z AG017310 Homo sapi AG017312 Homo sapi BH094331 RPCI-24-3 BG694687 NLSC_iv06 AV836265
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12 10 10 9	1000	12011	122110	12 12 10 10 0
4425 4425 4451 4557	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	529 537 543 552 552	5564 571 617 629 634 635	635 637 646 673 688
885.6 85.6 85.6	88888 885 895 895 895 895 895 895 895 89	888888 885 885 885 885 885 885 885 885	8888888 8856 8856 8856 8856 8856 8856 8	85.6 85.6 85.6 85.6
15. 15. 15. 15. 15. 15.	15.4	15.4 15.4 15.4 15.4 15.4	1155.4 1155.4 1155.4 155.4	15.4 15.4 15.4 15.4 15.4
118 220 221	226	32008	334 334 336 336	0 4 4 4 4 4 4 5 4 5 4 5 5 4 5 5 5 5 5 5
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BG531376 1441 bp mRNA linear EST 03-APR-2001 602559625F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4697383 5', mRNA sequence. BG531376.1 G1:13522913 FST. human. Human. Humo sapiens Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota, Metazoa; Chordata; Craniata; Hominidae; Homo.	ci.nih.gov of Health, ausberg, Pl. I.nih.gov Arcc ration: CLG ed by: The Incyte Ger Incyte Ger ingC clone.	http://image.llnl.gov plate: LicM1526 row: b column: 08 High quality sequence start: 186 High quality sequence stop: 226. Location/Qualifiers Location/Qualifiers location/Qualifiers / Organism="Homo sapiens" / Ab_xref="Laxon:9606" / Ab_xref="Laxon:9606" / Clone="InAGE:4697383" / Clone="Lib="MIH_MGC_61" / Lissue_type="embryonal carcinoma" / Lissue_typ	
RESULT 1 BG531376/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES	

Query Match

Matches

DEFINITION

BF516695

RESULT

g

ACCESSION

KEYWORDS

SOURCE

VERSION

ORGANISM

TITLE JOURNAL

FEATURES

REFERENCE AUTHORS BASE COUNT

BASE COUNT

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/note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: Xhor The library is from early (spring) secondary wood, taken from a ten year old tree in the transitional phase. The tree is a kind gift of the Westvaco Corporation. Secondary xylem was harvested from the tree by peeling back the bark and primary xylem and then removing the underlying tissue with a block plane. NoTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCACGAG'."

a 102 c 117 g 150 t 19 others
                                                                                                                                                                                                                           EST 26-FEB-2001
                                                                                                                                                                                                                   BG318395 513 bp mRNA linear EST 26-FEB-2003 NXPV_013_B06_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda cDNA clone NXPV_013_B06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 16-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 513)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="Coastal plain loblolly pine from North Carolina"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HS_3019_B2_R05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3019 Col=10 Row=L, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Clone_lib="NXPV_013_B06"
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/Clone_lib="NXPV (Nsf xylem Planings wood Vertical)"
/Csll_type="fylanings (secondary)"
/dev_stage="Transitional"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.4; DB 10; Length 513;
Pred. No. 4.5e+02;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pinus taeda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3352"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="XL1-Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    BG318395.1 GI:13127825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ621441.1 GI:5083833
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94.48;
                                                                 237 ATACACTGGTCATGTTAA 254
                                     1 atactctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 ATACACTGGTCATGTTAA 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     loblolly pine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      Pinus taeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sederoff, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
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                                                                                                                                                                                                                                           DEFINITION
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ORIGIN
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                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AQ621441/c
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                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                     BG318395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form side wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the sides of the inclined stems, and a mixture of all three genotypes was used for the library. Oligo-dr primed cDNA was directionally cloned into the EcoRI Thos genotes contain a 'CDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGAGGAG',"

80 a 74 c 75 g 103 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF516695

NXSI_002_C09_F NXSI (Nsf Xylem Side wood Inclined) Pinus taeda cDNA clone XXSI_002_c09 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NXSI_002_C09"
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/cell_type="Xylem"
/dev_stage="Juvenile"
/lab_host="Xil-Blue"
/note="Vector: BlueScript SK; Site_l: Eco RI; Site_2: XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
1 (bases 1 to 344)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
                sequence: 5'-ATTCTAGAGGCCCAGGCGCCACATG-dT(30)BN 3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                          94.4%; Score 17; DB 10; Length 1441; 100.0%; Pred. No. 3e+02; tive 0; Mismatches 0; Indels (
                                                                                                                                                                                                             1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ajohnson@unity.ncsu.edu
                                                                                                                                                                                                     367 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
adaptor sequence:
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                                                                                                                                                                                Library."
381 c
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                                                                                                                                                                                                                                                                                                                                                          17; Conservative
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Fax: 919 515 7801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: T3.
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Best Local Similarity
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91.1%; Score 16.4; DB 10; Length 571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
                                                          High quality sequence stop: 564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: ajohnson@unity.ncsu.edu
Plate: 41 row: L column: 24
Seq primer: SP6
Class: BAC ends
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1. .571
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94.4%;
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Best Local Similarity 94.4'
Matches 17; Conservative
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Pinus taeda
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BG318023
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                                             Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 564)

Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray Hood, L. Ettensohn, C.A., Lehrach, H., Britten, R.J. Davidson, E.H. and Hood, L.
                                                                                                                                                                                 High Throughput Sequencing Center
University of Mashington
University of Mashington
University of Mashington
Tell: (206) 616-3618
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3019 row: L column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .558
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3019 Col=10 Row=L"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
          1 (bases 1 to 558)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-coli DH10B"
                                                                                     Sequence-tagged connectors: A sequence approach to mapping and
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
                                                                                               scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cameron, RA, Davidson, EH, Hood, L
Division of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                    Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         150 t
                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 558.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ144687.1 GI:8296590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17; Conservative
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AUTHORS
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1. .564
/organism="Strongylocentrotus purpuratus"
/db_xref="taxon.7668"
/db_xref="Plate=1.01=24 Row=L"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                  ó
                                                                                                                                                                                                                                                                                                                                                                                   EST 26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                 NXPV_008_F06_F NXPV (Nsf Xylem Planings wood Vertical) Pinus taeda cDNA clone NXPV_008_F06_5', mRNA sequence.
BG318023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Coastal plain loblolly pine from North Carolina" /db_xref="taxon:3352"
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                                                                                                                                  6 others
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Pred. No. 4.6e+02;
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DEFINITION AZ207084/c

RESULT

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ACCESSION

KEYWORDS

VERSION

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 404)
Mahalras,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW812504 635 bp mRNA linear EST 17-MAY-2000 CM4-ST0181-231199-049-b12 ST0181 Homo sapiens CDNA, mRNA sequence.
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1 (bases 1 to 635)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Mala,G.S., Simpson,D.H., Brunstein,A., deolivaira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="Plate=3203 Col=24 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-5518
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW812504.1 GI:7905498
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Fax: +55-11-2707001
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Class: BAC ends
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                Homo sapiens
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Matches 16; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                           REFERENCE
                                                                                                                    AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                      SP_0127_A2_G12_T7A Strongylocentrotus purpuratus, purple sea urchin spenomic BAC library Strongylocentrotus purpuratus genomic clone Plate=127 Col=24 Row=M, DNA sequence.
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R., Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HE 2003_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=24 Row=E, DNA sequence.
AQ150695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strongylocentrotus purpuratus.
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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94.4%; Pred. No. 4.7e+02;
tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Davidson, EH, Hood, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strongylocentrotidae; Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="Plate=127 Col=24 Row=M"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Cameron, RA, Davidson, EH,
Division of Biology 156-29
California Institute of Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 724.
Location/Qualifiers
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Seg primer: T7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
                                                                                                                                                                                                                                                                                                                                                                                                   AZ207084.1 GI:8418313
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                                                                                1 atactctggtcatgttaa 18
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                           17; Conservative
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Matches 17; Conservative
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  Best Local Similarity
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DEFINITION

ACCESSION

KEYWORDS

SOURCE

VERSION

8

RESULT

AQ150695

BASE COUNT

ORIGIN

FEATURES

Gaps

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Seq primer: M13 Forward
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Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                3 actctggtcatgttaa 18
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                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone_lib="$$$70181"
/dev_stage="Adult"
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtmil2.pl?tl=&t2=CM4-ST0181-231
199-049-bl2&t3=1999-11-23&t4=1)
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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1 (bases 1 to 1026)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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Pred. No. 7.6e+02;
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                                                                                                                                                                    Seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence stop: 586.
                                                                                                                                                                                                                                                                             Location/Qualifiers
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Matches 16; Conserv
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Analysis of the recommensial with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CTOs polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CTOs library is a non-normalized library constructed from the following rat brain tissues: embryonic day 17, embryonic day 19, embryonic day 21, adult day 1, adult day 1, adult day 1, adult day 200. For a detailed description of the library from which this clone was derived, please visit our web site at ratest-eng-ulowa-edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 bp mRNA linear EST 19-JUL-200 LI-R-CT0S-cax-d-05-0-UI.sl UI-R-CT0S Rattus norvegicus cDNA clone DI287040
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: msoarcs@blue.weeg.ulowa.edu
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the non-normalized rat brain pool library cDNA Library Preparation:
M.B. Soarcs Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               451 Eckstein Medical Research Building Iowa City, IA 52242, USA
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/clone_11b="UI-R-CT0s"
/dew_stage="ADULT"
/lab_host="DH10B (Life Technologies)"
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="163022"
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Program for Rat Gene Discovery and Mapping
University of Iowa
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.plrtl=&t2=CM3-HT0143-220 Seq primer: puc 18 forward High quality sequence start: 102 High quality sequence start: 102 Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 225)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/db_xref="taxon:9606"
/clone_lib="HT0143"
/dev_stage="Adult"
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P. Nishiyama.Y. Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length CDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                        BB024447 RIKEN full-length enriched, adult male pituitary gland Mus musculus cDNA clone 5330421N15 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="RIKEN full-length enriched, adult male
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/dev_stage="adult"
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L. J. (JASSAS, 1.0.) JULY, Akahira, S., Akiyama, J., Arakawa, T., Carninci, F. Konno, H., Flakuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Toh, M., Hirozane, T., Horit, F., Ishi, Y., Kaya, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, F., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Takahashi, F., Tominaga, Y., Suzuki, H., Yausuki, H., Yausuki, H., Watanaba, S., Yamamura, T., Tyano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshino, RIKEM Mouse ESTS (Konno, H., et al.)
trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation carninci, P. and Hayashizaki, Y.
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URL:http://genome.gsc.riken.go.jp/
URL:http://genome.gsc.riken.go.jp/
Carninci,b., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Murama,Y., M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST 09-JUL-2000
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BB289468 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA clone B020040F24 3', mRNA sequence.
BB289468 GI:8989917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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The Institute of Physical and Chemical Research (RIKEN)
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94.1%;
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Best Local Similarity 94.1
Matches 16; Conservative
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KEYWORDS

VERSION SOURCE

ORIGIN

COMMENT

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BF147142
uy07f02.y1 McCarrey Eddy spermatocytes Mus musculus cDNA clone
IMAGE:3657339 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter. E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                           /note==Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] GAGAGAGARCCAAGGACTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 337)
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                       Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                          /clone_lib="RIKEN full-length enriched, 2 cells egg"
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/dev_stage="2 cells"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                              /organism="Mus musculus"
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Location/Qualifiers
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Matches 16; Conservative
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Fax: 314 286 1810
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KEYWORDS
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FEATURES

source

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/issue_type="spermatocytes, pooled from multiple mice"
/dssue_type="spermatocytes, pooled from multiple mice"
/dab_host="DH10B (phage-resistant)"
/note="organ: testis; Vector: pBluescript SK+ (Stratagene)
): Site=1: XhoI: Site=2: EcoRI: cDRA oligo dT-primed
]: Site=1: XhoI: Site=2: EcoRI: cDRA oligo dT-primed
[5'-(GA)10-ACTAGCTCGGGTTTTTTTTTTTTTT] and directionally
cloned using 5' linkers 5'-AATTGGCACGAC3' and
S'-CTCGTGCCG-3'. Size selection of >400bp material gives
average insert size ranging from 1-2 kb. Library was mass
excised (from lambda-UnizAP-XR) and resulting
single-stranded phagemids were prepped and tranformed
into DH10B. Library contains 90% recombinates.
References: J. Androl. 20:635-639 and Gene 25:263-269.
Library constructed and donated by J. McCarrey, Ph.D.
(Southwest Foundation for Biomedical Research, Dept. of
Genetics); excision done by E.M. Eddy, Ph.D. (National
Institutes of Health, National Institute of Environmental
Health Sciences). Original lambda-based library is
available through ATCC, catalog #63422."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                    /clone_lib="McCarrey Eddy spermatocytes" /sex="male"
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/db_xref="taxon:10090"
                                                                                                /clone="IMAGE:3657339"
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Matches 16; Conservative
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Search completed: July 31, 2002, 12:12:16 Job time: 13489 sec

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July 31, 2002, 14:11:25; Search time 720.8 Seconds (without alignments) 42.875 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
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Sequence 32167 BP; 9824 A; 5983 C; 6230 G; 10130 T; 0 other;
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DB 21; Length 44848;

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Query Match Best Local Similarity

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                                                                                                                                               Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
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07-JUN-2000;
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2000US-0241826
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17-NOV-2000;
08-SEP-2000;
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amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. (1) expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynuclectides may be used to produce the secreted (1), by inserting the nonleic acids into a host cell and culturing the cell to express the proteins and polynuclectides may be used to produce the secreted (1), by inserting protein. (1) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 23323; 3071pp + Sequence Listing; English.
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2000US-0251479.
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2000US-0251989.
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
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08-DEC-2000;
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AAK57354/c
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cytostatic; gene therapy; vaccine; metastasis; ss.

-2000); 2000US-02354842000); 2000US-02358842000); 2000US-02358842000); 2000US-02358842000); 2000US-02358842000); 2000US-02363672000); 2000US-02363892000); 2000US-02363892000); 2000US-02363892000); 2000US-02363892000); 2000US-0236992000); 2000US-0236992000); 2000US-023992000); 2000US-023992000); 2000US-023992000); 2000US-02418092000); 2000US-02418092000); 2000US-02418092000); 2000US-02464772000); 2000US-02464782000); 2000US-02466102000); 2000US-02466112000); 2000US-02466112000); 2000US-02466112000); 2000US-02466112000); 2000US-02466112000); 2000US-02466112000); 2000US-02466112000); 2000US-02465292000); 2000US-02465292000); 2000US-02492112000); 2000US-0249211.	-2000; 2000US-0251988 -2000; 2000US-0256719 -2000; 2000US-0251479 -2000; 2000US-0251866 -2000; 2000US-0251868 -2000; 2000US-0251869 -2000; 2000US-0251869 -2000; 2000US-0251990 -2000; 2000US-0251990 -2000; 2000US-0251699
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AAK64951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased cappraclectides may be used to production of (I). Additionally, (I) polynuclectides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynuclectides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 ccancers and cancer metastases of haematopoietic-derived cells. AAK64703 sequences from the present invention AAK6442 to AAK64803 and AAM83169
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                                                                                                                                                                                                                                                                                                                                              represent sequences used in the exemplification of the present invention.
                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                                                                        82.2%; Score 14.8; DB 22; Length 407;
88.9%; Pred. No. 2.4e+02;
Live 0; Mismatches 2; Indels 0;
                                                                                                                                Claim 1; SEQ ID NO 2414; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                      Sequence 407 BP; 105 A; 102 C; 56 G; 140 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; vaccine; metastasis; ds.
                           Barash SC, Ruben SM;
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2000US-0198123.
2000US-0205515.
 (HUMA-) HUMAN GENOME SCI INC.
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Matches 16; Conservative
                                                 WPI; 2001-483426/52.
                                                            P-PSDB; AAM84573
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16-MAR-2000;
17-MAR-2000;
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19-MAY-2000;
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2000US-0216647
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20-0CT-2000;
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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
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2000US-0246525.
2000US-0246526.
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expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haemacopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 cancers and cancer metastases of haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK54950 and AAM81269 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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88.9%; Pred. No. 2.5e+02;
ive 0; Mismatches 2; Indels 0)
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Matches 16; Conservative
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynucleotides may be used in the prevention, diagnosis and
cexample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
polynucleotides may be used to produce the secreted (I), by inserting
the nucleic acids into a host cell and culturing the cell to express the
protein. (I) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
concers from the present invention. AAK54942 to AAK5459 and AAM82169
represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                     2000US-0249210.
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82.2%; Score 14.8; DB 22; Length 474; 88.9%; Pred. No. 2.5e+02; Live 0; Mismatches 2; Indels 0;

Query Match 82.29 Best Local Similarity 88.99 Matches 16; Conservative

Sequence 474 BP; 135 A; 109 C; 90 G; 140 T; 0 other;

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The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTS are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the Same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production of the global expression of genes from FF cells allows the production collscovered, possible functions of unknown open reading frames can be described and gene copy number variation and stability can be identified and gene copy number variation and stability can be despribled and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore compinearing. Using ESTS provides several advantages over genomic or array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate conditions, analysis of the results. AAF01247 represents ESTS from the procession of from inverse to stability the procession of from inverse to stability the procession of from the procession of from inverse to stability the procession of from the procession of from inverse to the procession of from the 
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                                                                                                                                                                                                                                                                                                                                                                                              Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss.
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                                                                                                                                                                                    AAF10198 standard; cDNA; 596 BP
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82.2%; Score 14.8; DB 21; Length 596;

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                                1 atactctggtcatgttaa 18
                                                                                                                            (first entry)
                 16; Conservative
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                                                                                                                                                                                             Arabidopsis thaliana
       Best Local Similarity
Matches 16; Conserve
                                                                                                                                                                                                              EP1033405-A2.
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06-APR-1999;
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                                                                                                                                                                                                                                                                                09-MAR-1999
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                                                                                                           AAC33932;
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	Gaps
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	Length
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20 MAY - 1999;
24 MAY - 1999;
25 MAY - 1999;
27 MAY - 1999;
28 MAY - 1999;
01 - JUN - 1999;
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RESULT
AAC34572
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us-09-899-718a-8.rng

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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17-OCT-2000 (first entry)
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07-JUN-1999;
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14-JUN-1999;
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16-JUN-1999;
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06-MAY-1999;
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07-MAY-1999;
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05-MAR-1999;
09-MAR-1999;
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04-MAY-1999;
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30-APR-1999;
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88.9%; Pred. No. 2.7e+02;
Live 0; Mismatches 2; Indels 0;
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31-AUG-1999;
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Best Local Si
Matches 16;
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Gaps
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Best Local Similarity 88.99
Matches 16; Conservative
27-AUG-1999;
27-AUG-1999;
30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
10-SEP-1999;
13-SEP-1999;
13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
16-SEP-1999;
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12-0CT-1999;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (and pharmaceutical drugs. The invention sequences (ABLI6175) and the encoded proteins
                                                                                                                     New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                         (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition; papilla; contact site; callose; carbohydrate; phenol; transgenic plant; Mlo; Erysiphe graminis; powdery mildew; ss.
                                                                                                                                                                                                                                                                                                                                               82.2%; Score 14.8; DB 23; Length 1926;
88.9%; Pred. No. 2.8e+02;
tive 0; Mismatches 2; Indels 0;
                                                                                                                                                             Claim 1; SEQ ID NO 29374; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana Mlo fungal resistance gene CIB10295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "Mlo fungal resistance protein"
                                                                                                                                                                                                                                                                                                             Sequence 1926 BP; 394 A; 531 C; 565 G; 436 T; 0 other;
                                                                                  Li PWD, Myers EW;
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
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                         23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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Matches 16; Conservative
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                                                                              Venter JC, Adams M,
                                                                                                   WPI; 2001-656860/75.
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Pred. No. 2.8e+02;
0; Mismatches 2; Indels 0;
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ID ABL25967 standard; DNA; 1926 BP.
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les 16; Conservative
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04-OCT-1999;
05-OCT-1999;
06-OCT-1999;
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13-OCT-1999;
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Gaps

Kramer CM;

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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                          Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae; powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel polynucleotide which encodes Mlo protein from wheat, useful for producing fungal resistant plants, in particular wheat plant
                                                                                      This sequence represents the coding region for the Arabidopsis thaliana fungal resistance gene CIB10295. The Mio protein confers resistance to fungal resistance by stimulating the formation of large cell wall appositions, designated papillae, at the conteact site with the fungal pathogen. These papillae mainly contain callose, but also contain pathogen. These papillae mainly contain callose, but also contain carbohydrate, phenols and proteins and are used to prevent penetration of the fungal hyphae into the plant. The new Mio sequences are used to generate transgenic plants resistant to fungal pathogens, especially
                                                                                                                                                                                                                                            Gaps
                                           New proteins useful for generating transgenic plants resistant to
                                                                                                                                                                                                                      82.2%; Score 14.8; DB 20; Length 1935;
88.9%; Pred. No. 2.8e+02;
Live 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of the Arabidopsis Mlo protein CIB10295.
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                                                                                                                                                                                           Sequence 1935 BP; 576 A; 382 C; 398 G; 579 T; 0 other;
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Levin JZ, Heifetz PB, Patton DA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a //product= "Mlo protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
89..1810
                                                                             Claim 3; Page 78-81; 102pp; English.
                                                                                                                                                                             Erysiphe graminis (powdery mildew).
                                                                                                                                                                                                                                                                                                                                      AAF24587 standard; DNA; 1935 BP.
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Matches 16; Conservative
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                       WPI; 1999-571820/48.
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                                                               fungal infection
                                    P-PSDB; AAY26970.
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Vernooij BT,
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The present sequence encodes a Mlo protein. Mlo proteins given resistance to fungal pathogens which infect living epidermal plant cells. Mlo proteins give proteins resistance to fungal pathogens, especially Mlo proteins give proteins resistance to fungal pathogens, especially rerysiphe graminis (powdery mildews). In barley, mutations at the Mlo Erysiphe graminis (powdery mildews). In barley, mutations at the mochanism locus are responsible for a plant resistant pathotype. The mechanism of Mlo resistance involves the formation of large cell wall appositions, of Mlo resistance involves the formation of large cell wall appositions callose, but also carbohydrates, phenols and proteins. Polynucleotides encoding Mlo proteins are useful for making transgenic plants, preferably wheat, which are resistant to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0225757.
2000US-0225758.
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2000US-0180628.
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AMESA951 to AAK64702 encode the human immune/haematopoiettc antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased that affect the activity of (I) by expressing inactive proteins or complement the patients own production of (I). Additionally, (I) explained the proteins or to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the concers and cancer metastases of hematopoietic-related diseases, especially cancers and cancer metastases of hematopoietic-derived cells. AAK64703 concers from the present invention. AAK54912 to AAK87650 and AAM82169 very represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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Description

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cambridgeshire. CBIO 1SA, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

nov 17, 2001 this sequence version replaced gi:15721150.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

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S1019 bp DNA linear VRT 23-JAN-2002

Sebrafish DNA sequence from clone XX-221H6 on chromosome 7 Contains a novel gene similar to nitr3r.1 (novel immune-type receptor 3r.1), a novel gene similar to nitr3 and part of two novel genes similar
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Patent: WO 0202785-A 1 10-JAN-2002;
Aventis CropScience GmbH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; immune-type receptor; nitr3; nitr3r.l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       961 t
                                                    0; Mismatches
                                9
                                                                                                                                                                                                                                                                            3785 bp
Sequence 1 from Patent WO0202785.
AX349063
                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to nitr's, complete sequence.
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AL591420.5 GI:16973933
                                                                                                                                                                                                                                                                                                                                                                    AX349063.1 GI:18615098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 atactctggtcatgttaa 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o 086
                                   100.08;
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                                                                                                                1 atactctggtcatgttaa 18
                                                                                                                                           1 ATACTCTGGTCATGTTAA 18
                                                                 Conservative
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                                      Best Local Similarity
Matches 18; Conserv
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                     Query Match
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ORIGIN
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                              DEFINITION
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RESULT

7

REFERENCE AUTHORS JOURNAL

KEYWORDS

VERSION

AX349063

RESULT

δλ

FEATURES

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)=
chemistry or covered by high quality data (i.e., phred quality)=
30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the abbreviations are used to associate primary accession numbers given abbreviations are used to associate primary accession numbers given symptement table with their source databases: Em., EMBL; Sw., in the feature table with their source databases: Em., EMBL; Sw., database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep XX-221H6 is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MSLQDCFTFFLLTFAYGTCEEDFIHQQPLVVAELGSSVTLPCFH SDDFITTISHYKHSAGKKFLLTAFANNSGSVTYQYAFNNTNRFFTTASGSVTLSTL SHLEKEDFANYYCAKFFLNIMMFGEGTTLLHNETDRNISTSYSAPSFWTPVVCILLIS VISTYMNIVLVIGSRKKFTTEQLRSQINQIKTDDLNYAALHFSKTKPFTSRRSSMKT 10ETIYSETTVH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /evidence=not_experimental
/product="SC:dZ221H6.1 (novel immune-type receptor similar
                                                                                                                                                                                                                                                                                                                                        VECTOR: pCYPAC-6

WECTOR: pCYPAC-6

It may be shorter because we sequence overlapping sections only

It may be shorter because we sequence overlapping sections only

once, except for a short overlap,

once, except for a short overlap.

The true right end of clone XX-221H6 is at 51019 in this sequence.

The true right end of clone XX-139B19 is at 2000 in this sequence.

This clone was isolated from the BUSM1 library (C. Amemiya) and

provided by C. Amemiya (Amemiya lab, Virginia Mason Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inconsistency in the number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2825,3152. .3505,4439. .4573,5294. .5328,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="23 copies 4 mer tata 91% conserved"
/note="23 copies 4 mer tata 91% conserved"
join(2780. .2825,3152. .3505,4439. .4573,5294. .5328,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anote-"mandem repeat. Inconsistency in the numb copies of the repeat element between subclones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5902. .5959
/note="29 copies 2 mer at 81% conserved"
7894. .7919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="16 copies 4 mer atat 75% conserved"
588. .631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      match: proteins: Tr:CAD12598 Tr:AAK60113"
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/note="32 copies 2 mer tt 62% conserved"
4000. 4019
/gene="SC:d2221H6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              copies 2 mer ta 86% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="50 copies 2 mer ta 91% conserved"
1163. 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4019. .4060
/notes="3 copies 14 mer 100% conserved"
complement(4020. .4061)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mononucleotide run between subclones.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 copies 12 mer 86% conserved"
1256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: cDNAs: Em:AF318401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAD21620.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SC:dZ221H6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:7955"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'gene="SC:dZ221H6.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="Amemiya"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="XX-221H6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .5796)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center, Seattle, USA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="22
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Action of 29, 2001 this sequence version replaced g1:14529902.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., pirce quality >= as compressions and repeats, all regions were covered by at least as sembly was confirmed by restriction digest. The following absentions are used to associate primary accession numbers given swissembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given swissembly the feature table with their source databases: Em:, EMBL; Sw:, Swissprot; Tr:, TrembL; Wp:, WORMPEP: Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL512443 55613 bp DNA linear PRI 26-OCT-2001
Human DNA sequence from clone RP11-108P2 on chromosome 1, complete
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-02T-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                 /note="TDR1 repeat: matches 727. .934 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="DANA repeat: matches 147. .406 of consensus" 27825. .27883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="DANA repeat: matches 1. .59 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 5; Length 51019;
                         /note="29 copies 2 mer ga 69% conserved" 19721. .19776 /note="4 copies 14 mer 80% conserved" 21020. .21227
                                                                                                                                                           21332, 21377

/note="23 copies 2 mer aa 80% conserved"

21756, 21803

/note="4 copies 12 mer 91% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="23 copies 2 mer ta 80% conserved"
23406. .23531
                                                                                                                                                                                                                                                                                                                                             /note="17 copies 2 mer ca 97% conserved" 22702. .22867
/note="match: STS: Em:G41123" 22912. .22957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="36 copies 2 mer aa 66% conserved" 27596. .27827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="6 copies 21 mer 70% conserved" 23996. 24067 /note="6 copies 12 mer 100% conserved" 25897. 25968
                                                                                                                                                                                                                                                                                             /note="match: STS: Em:G39804"
22354. .22387
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                                                                                                                                                                                                                                                                      .22528
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AL512443.7 GI:16508240
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Matches 17; Conservative
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join(17884. 17929,18244. 18597,20317. 20670,20748. 20846,
21488. 21523,21967. 22089)
/gene="Sc:dz221H6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(17884...17929,18244...18597,20317...20670,20748...20846,
21489...21523,21967...22089)
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                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="GTCEEDFIHQOPLVLAELGSSVTLPCFHSDDFVTTISWYKHSAG
KRPLLIAYSDFNSGRVTYRNAFNNTNRFFITVASGSYNLTIIHLEKEDFATYYCVKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence-not_experimental
/product="Sc:d2221H6.3 (novel immune-type receptor)"
/product="Sc:d2221H6.3 (novel immune-type receptor)"
/db_xref="G1:18369623"
/db_xref="G1:18369623"
/ftanslation="ETDRISSTSVIQOPVSDRLHPGDSVTLQCSVSSHICAGHYRVYW
FKHSGYSQPGIIYTHDNRSDQCLESSERSSFVQSCVYSLSGTEJTTSDAGVYYCAVD
FCGKIRRGNGTRLTTERSSLAMSPVLILEVISAVSIIVNIFLIIRTYCKE"

Complement(13097. 13274)
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/db_xref="G1:18369624"
/translation="MSLOSSTFFFLIFAYGTCEEDF1HQOPLVVAELGSRVTLPCFH
SDDYTTVSWWTKHSAGKFPLLIAYSDFNSGRYTYQNAFWWNNRFFTTVASGSYNLTII
HLEKEDPATYTCVKDFLNAFGEGTILLRKETDRISSTSVIQQPYGDRLHGGSYTL
QCSVSSHICAGHYRVYWFKRSSGSYSGFITTHNREDQLESSEKSSRYSOSSYSILS
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LVLONRRKETTEQLRGQINQIETDDLNYAALHFSKTKPSTSRRSSIKTIQETIYSETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: CDNAs: Em:AP318388 Em:AF318400 Em:AF318399 match: proteins: Tr:AAK6106 Tr:CAD12509 Tr:CAD12585 Tr:AAK60110 Tr:AAK60112 Tr:CAD12599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
/product="SC:dZ221H6.4 (novel immuntype receptor similar
to nitr3)"
                                                                                                                                                                                 /note="predicted by Pfam
match: proteins: Tr:CAD12524 Tr:CAD12506 Tr:CAD12582
                                                                                                                                                                                                                                                                                          /evidence=not_experimental
/product="SC:dZ221H6.2 (novel immune-type receptor)"
/protein_id="CAD21621.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted by pfam
match: proteins: Tr:AAK60111 Tr:AAK60112 Tr:CAD12599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="DDNA repeat: matches 322. .405 of consensus"
join(10373. .10727, 10812. .10913)
/gene="Sc:d221H6.37"
join(210373. .10727, 10812. .>10913)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOZ/9. 100/4
Jobes 10602
Jobes DANA repeat: matches 89. .406 of consensus"
/note="DANA repeat: matches 5. .59 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19173. .19252
/note="DANA repeat: matches 322. .405 of consensus"
19325. .19382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"DANA repeat: matches 10. .377 of consensus"
16279. .16574
'note="13 copies 2 mer tt 100% conserved"
                   3572. .8637
/note="33 copies 2 mer tt 68% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="32 copies 2 mer tt 70% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Join(<10373. .10727,10812. .>10913)
/gene="SC:dz221H6.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: STS: Em:G40916"
14549. .14869
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:18369622"
                                                                                                     /gene="SC:dZ221H6.2"
                                                                                                                                                           /gene="SC:dZ221H6.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNRLMFGEGTILLCK"
                                                                                                                                                                                                                                                                   /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                    .>899
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                      repeat_region
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 4, clone RP11-85D17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:01855
fragment_chain:1"
52785, .K6125
                                                                                                                                                                                                                                                /note="assembly_fragment:01316
fragment_chain:1"
3250. 14161.
/note="assembly_fragment:00988
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment:01272
fragment_chain:1"
32798. .52684
                                                                                                                                                                                                                                                                                                                                                                                                                                 25407. .29595
/note="assembly_fragment:01886
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:01033
fragment_chain:1"
                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment:01324
fragment_chain:1"
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                                                                                                                    /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                                             /clone_lib="Amemiya"
                                                                        Location/Qualifiers
                                                                                                                                                                                      /clone="XX-27N24"
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                                                                                                                                                                   /chromosome="1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .32697
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                                                                                                                                                                                                                                .3149
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                                                                                                                                                                                          IMPORTANT: This sequence is not the entire insert of clone RP1-108P2 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-38609 is at 53614 in this sequence. The true right end of clone RP3-333A15 is at 2000 in this sequence. Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGRP4; version 4.5
Assembly program: XGRP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Sequencing vector: plasmid; L08752; 100% of reads
Consensus quality: 72055 bases at least 040
Consensus quality: 72273 bases at least 030
Consensus quality: 72397 bases at least 020
Insert size: 72609; sum-of-contigs
Insert size: 88868; 5.6% error; agarose-fp
Quality coverage: 11.34x in Q20 bases; sum-of-contigs Quality
coverage: 9.50x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submitted (19-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 21, 2001 this sequence version replaced gi:15626247.
                                                                                      http://www.sanger.ac.uk/HGP/Chrl
RPI1-108P2 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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18193 a 10125 c 9972 g 17323 t
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                       /db_xref-"taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="1
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Matches 17; Conservative
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2 (bases I to 81017)
2 (bases I to 81017)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Barren, B., Linton, L., Badar, F.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslaviy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campopiano, A., Castle, A., Chopel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S.,
Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 4 clone RP11-85D17 map 4, LOW-PASS SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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* NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Levine, R., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J.,
McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mercheeters, R.,
Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J.,
Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donneil, P.,
Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
Stange-Thomann, N., Stojanovic, N., Subreamanian, A., Talamas, J.,
Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Direct Submission, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                       Submitted (03-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA all repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 94 individual
* sequencing reads that have not been assembled into
* contigo. Runs of N are used to separate the reads
* and the order in which they appear is completely
* identifying clones sequence sampling is useful for
* overlap relationships among clones to be deduced.
* However, if should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8467: contry or for a gap of 100 bp 9320: contry of 753 bp in length 120: gap of 100 bp 10187: contry of 767 bp in length 1087: gap of 100 bp in length
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gap of 100 bp
1567: contig of 758 bp in length
7: gap of 100 bp
7.337: contig of 766 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5999: gap of 100 bp 6764: contig of 765 bp in length
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11142: gap of 100 bp
11910: contig of 768 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project Information
Center project name: L7756
Center clone name: 85_D_17
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; gap of
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7612;
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19475: gap of 100 bp 10
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5349 15448: gap of 100 bp
5449 16206: contig of 758 bp in length
6207 16306: gap of 100 bp
                                                                                                                     contig of 748 bp in length
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                                                                                                                                                                                         contig of 746 bp in length
                                                                                                                                                                                                                17901 18000: gap of 100 bp
18001 18767: contig of 767 bp in length
                                                                                                                                                                                                                                                                                        167: gap of 100 bp 19642: contig of 775 bp in length 42: gap of 100 bp 20493: contig of 751 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                        21337; contig of 744 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37: gap of 100 bp
22202: contig of 765 bp in length
02: gap of 100 bp
23072: contig of 770 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72: gap of 100 bp
23941: contig of 769 bp in length
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35216: contig of 779 bp in length
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17900: cont
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26515: cont
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28238: cont
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29104: con
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43030: conf
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105939 bp DNA linear HTG 20-DEC-2001
Rattus norvegicus clone CH230-6L20, *** SEQUENCING IN PROGRESS ***, ACOMAGAE PIECES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                  55154: gap of 100 bp
55921: contig of 767 bp in length
56021: gap of 100 bp
56781: contig of 760 bp in length
56881: gap of 100 bp
57638: contig of 757 bp in length
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58: 5504: contig of 756 bp in length
54: gap of 100 bp
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                                                                                                                                                                                                                                                                                                                     27: gap of 100 bp 54198: contig of 771 bp in length
                                                                                                                                                                                                                                                                                         73: gap of 100 bp
53327: contig of 754 bp in length
                               47341 47440: gap of 100 bp
47441 48111: contig of 731 bp in length
4812 48271: gap of 100 bp
48772 49028: contig of 757 bp in length
                                                                                                          p of 100 bp contig of 755 bp in length
                                                                                                                                                            49983: gap of 100 pp
50748: contig of 765 bp in length
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47340: contig of 753 bp in length
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59364: cont
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Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L. Li, J., Li, L., Li, Lu, J., Lid, W., Loulesged, H., Lozado, R.J., Luix, Lucier, A., Lucier, R., Luna, R., Loulseged, H., Lozado, R.J., Maria, R., Martin, R., Martingla, R., Martin, R., Martingla, R., Marting, R., Moordan, M., Mossey, M., Moser, M., Neal, D., Newtson, J., Newtson, N., Neyten, N., Nickerson, E., Naokenkwo, S., Nuyen, A., Nguyen, N., Nickerson, E., Naokenkwo, S., Oguh, M., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Petery, J., Perez, L., Peters, L., Spickens, R., Primus, E., Pu, L.L., Ruiz, S., Savery, G., Scherter, S., Scott, G., Shen, H., Shtoshtari, N., Stone, H., Sutton, M., Savtek, A., Taylor, T., Talfrod, B., Thomas, N., Taylor, C., Taylor, T., Talfrod, B., Thomas, N., Tang, H., Tansey, J., Taylor, T., Talfrod, B., Thomas, N., Tang, H., Tansey, J., Taylor, T., Talfrod, B., Thomas, N., Thomas, S., Warren, R., Washington, C., Wall, R., Wu, X., Washington, C., Walliams, G., Wall, R., Wu, X., Washington, S., Wall, R., Wu, Y., Williamson, A., Wilestyk, R., Wooden, S., Warren, R., Wall, R., Wu, X., Wall, R., Wall, R., Wall, R., Wu, Y., Wall, R., Wall, Wall, R., Wall, Wall, R., Wall, R
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* (see http://www.hgs.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* consists of 56 contigs. The true order of the pieces

* consists of 56 contigs. The true sequence record is

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence.
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Direct Submission
Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department Submitted (15-SEP-2001) Human Genetics, Baylor College of Medicine, One of Molecular and Human Genetics, Baylor College of Medicine, One Havlor Plaza, Houston, TX 77030, USA
Ravlor Plaza, Houston, TX 77030, USA
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On Dec 20, 2001 this sequence version replaced gi:17062175.
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Contact: hgsc-help@bcm.tmc.edu
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Felis catus clone RP86-117J4, WORKING DRAFT SEQUENCE, 8 unordered
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Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W.,
Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S.,
Guan, X., Gupta, J., Ho, S.-L., Idol, J.R., Karlins, E., Lee-Lin, S.-Q.,
Legaspi, R., Lim, M., Maduro, Q.L., Maduro, V.B., Massiello, C.,
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Mammalia, Eutheria: Carnivora, Fissipedia, Felidae, Felis.
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104544: contig of 1035 bp in length
104644: gap of unknown length
105939: contig of 1295 bp in length
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gap of unknown la
contig of 1894 b
gap of unknown la
gap of unknown la
contig of 1884 b
gap of unknown la
contig of 1888 b
gap of unknown la
gap of unknown la
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AC091696
AC091696.1 GI:14150418
HTG: HTGS_PHASEI; HTGS_DRAFI.
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94.48;
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94150:
94250:
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AL359456_0
AL359456_1
AL359456_2
AL359456_3
AL359456_3
AL359456_4
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AL359456_1
WPCOMMENT
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24909 35362: contig of 10454 bp in Lengtn
35363 35462: gap of 100 bp
35463 43765: contig of 8303 bp in length
                                                   Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Summary Statistics
                    47358. .72019
/note="assembly_fragment"
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vector_side:right"
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                                                                                                                                                                                                                                                                                                                              Db 65046 ATACTCTGGTCATGTTGA 65029
                                                                                                                                                                                                                                                                                         1 atactctggtcatgttaa 18
                                                                                                                                                                                                                   Query Match
Best Local Similarity 94.44
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Burton, J.
Direct Submission
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                                                                                                                                     37260 a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
            Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Frasad,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Zhang,L.-H. and Green,E.D.
                                                                                                                                                                                         Submitted (19-MAY-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 8 conigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 133000, agarose-fp agarose-fp agarose-fp (bality coverage: 11.63x in Q20 bases; agarose-fp quality coverage: 11.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                  sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality; 133760 bases at least 040 consensus quality; 134423 bases at least 030 consensus quality; 13418 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out of 10935 bp in length gap of unknown length contig of 16042 bp in length contig of 14662 bp in length contig of 24662 bp in length
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137140: contig of 34372 bp in length.
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gap of unknown length
contig of 6587 bp in length
gap of unknown length
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                                                                                                                                                                                                                                  Center: NIH Intramural Sequencing Center
                                                                                                                                                                                                                                                                                         Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
...----- Project Information
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/note="assembly_fragment
clone_end:T7
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/note="assembly_fragment"
13494. .20080
/note="assembly_fragment"
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47357:
72019:
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                                                                                                                       Unpublished
                                                                                                                                                                    Green, E.D
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HTG 19-DEC-2001
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Cambridgeshire, CB10 13A, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
humquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk
n Dec 20, 2001 this sequence version replaced gi:14133148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 10 clone RP13-143F22, *** SEQUENCING IN PROGRESS ***, 11 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGA44; version 4.5
Assembly program: XGA44; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye: 100% of reads
Consensus quality: 134134 bases at least Q40
Consensus quality: 137107 bases at least Q20
Consensus quality: 137107 bases at least Q20
Insert size: 137716; sum-of-contigs Quality
Insert size: 151380: 17.0% error; agarose-fp
Quality coverage: 5.19x in Q20 bases; sum-of-contigs Quality
coverage: 4.77x in Q20 bases; agarose-fp
                                                                                                                                                                                               Gaps
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                                                                                                                     91.1%; Score 16.4; DB 2; Length 137140; 94.4%; Pred. No. 95;
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                                                                                                                                                                                               1; Indels
709 others
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us-09-899-718a-8.rge

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Page

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                             1 (bases 10-147267)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
Unpublished
                                                                                                                                                                                                         2 (bases 1 to 147267)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
Submitted (16-OCT-2001) Genome Center, University of Washington,
Box 352145, Seattle, WA 98195, USA
On Oct 16, 2001 this sequence version replaced 91:7212074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: unknown; 65% of reads
Sequencing vector: plasmid; L08752; 35% of reads
Chemistry: Dye-terminator ET; 66% of reads
Chemistry: Dye-terminator ET; 66% of reads
Chemistry: Dye-terminator ET; 66% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 145614 bases at least Q40
Consensus quality: 146445 bases at least Q20
Consensus quality: 146882 bases at least Q20
Insert size: 147067; sum-of-contigs
Quality coverage: 9.4x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently * consists of 3 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 147267;
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                                                                                                                                                                                                                                                                                                                                                   Center: University of Washington Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: chr-3 (bc0228)
Center clone name: RP11-107K23 (bc0228)
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47259. 147267. 147267 / note="assembly_name:Contigl4"
45465 a 29529 c 28742 g 43321 t
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Pred. No. 96;
0; Mismatches
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/chromosome="3"
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94.48;
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                                              ORGANISM
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                                                                                                                                                             TITLE
JOURNAL
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147267 bp DNA linear HTG 16-000 sapiens chromosome 3 clone RP11-107K23, WORKING DRAFT SEQUENCE, 3 unordered pieces.

AC097356 AC024017

AC097356.1 GI:16152306

HTG: HTGS_PHASEI; HTGS_PRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.1%; Score 16.4; DB 2; Length 138716; 94.4%; Pred. No. 95; Live 0; Mismatches 1; Indels 0;
43766 43865; gap of 100 bp
43866 47699; contig of 3834 bp in length
47700 47799; gap of 100 bp
47800 78351; contig of 30552 bp in length
78352 78451; gap of 100 bp
78452 81539; contig of 3088 bp in length
81540 81639; gap of 100 bp
81640 88953; contig of 7314 bp in length
88954 89053; gap of 100 bp
                                                                                                                                                                                                                                 95325 95424; gap of 100 bp
95425 98902; contig of 3478 bp in length
98903 99002; gap of 100 bp
99003 138716; contig of 39714 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ture 99003. .138716
/note="assembly_fragment:01608"
45713 a 26430 c 25963 g 39610 t 1000 others
                                                                                                                                                                                   88954 89053: gap of 100 bp
89054 95324: contig of 6271 bp in length
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Tragment_chain:2"
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/clone_lib="RPCI-13.1"
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 8, 2000 this sequence version replaced 91:7630812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (08-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 148418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
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                                                                                                           PRI 09-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2. Description of the control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence was finished as follows unless otherwise noted:
                                                                          AC020698 148418 bp DNA linear PRI 09-M
Homo sapiens BAC clone RP11-45F23 from 5, complete sequence.
AC020698
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nguyen,C., Drone,K., Hawkins,M. and Ureta,M.
The sequence of Homo sapiens BAC clone RP11-45F23
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
..... Summary Statistics
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.G. and de Jong, P.G. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong

SOURCE INFORMATION:

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The clone sequenced to the left is RP11-462622. Actual start of this clone is at base position 1 of RP11-45F23; actual end is at base position 148418 of RP11-45F23. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="similar to EST BE087288 (NID:98477683)"
                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
NEIGHBORING SEQUENCE INFORMATION:
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/rpt_family="MER2_type"
23355. .2344?
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04107. .24873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="MER2_type"
                                                                                                                                                                                                                                                                                                                      rpt_family="MER2_type"
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/rpt_family="ERV1"
30745. .31712
                                                                                                                                                    /clone_lib="RPCI-11"
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29974. .30286
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30287. 30727
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?5372. .25522
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28790. .28843
                                                                                                                                    /clone="RP11-45F23"
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24873. 2520.
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31227. .31275
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33485. .23625
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31287. .22345
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807. .2585
/rpt_family="L1"
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.9869. .20177
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22727. .22937
                                                                                                                                                                             /rpt_family="L1"
507. .807
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251. 3596
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                                                                                                              /chromosome="2"
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repeat_region

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EST AA503255 (NID:g2238222) ng77a04.s1"
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                                                                                                                                                                                                                                                                                                                EST AA214188 (NID:91812807) zq90d03.s1"
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  91.1%; Score 16.4; 1
94.4%; Pred. No. 96;
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Query Match
Best Local Similarity
                    Matches
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Gaps

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standard; DNA; HTG; 164235 BP.
                        AC036175
                                                      AC036175;
RESULT 13
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RA Birren B., Linton L., Nusbaum C., Lander E., Abraham H., Allen N.,
RA Anderson S., Baldwin J., Barna N., Bastien V., Beda F., Boguslavkiy L.,
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RA Colangelo M., Collins S., Collymore A., Cooke P., Dearellano K., Dewar K.,
RA Diaz J.S., Dodge S., Domino M., Doyle M., Ferreira P., Fitzhugh W.,
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RA Liev I., Johnson R., Jones C., Kann L., Karatas A., Klein J., LaRoque K.,
RA Looke K., Macdonald P., Marquis N., Mercarthy M., McEwan P., McGurk A.,
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RA Stojanovic N., Subramanian A., Talamas J., Tesfaye S., Theodore J.,
RA Wilson B., Wu X., Wyman D., Ye W.J., Young G., Zainoun J., Zimmer A.,
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                               HOMO Sapiens chromosome 2 clone RP11-704A16 map 2, WORKING DRAFT SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (07-APR-2000) to the EMBL/GenBank/DDBJ databases. Whitehead Institute/MIT Center for Genome Research, 320 Charles Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 12, 2000 this sequence version replaced gi:7523843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently * consists of 19 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center Clohe name: 704_A_16

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155591 bases at least Q40
Consensus quality: 159816 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 168000; agarose-fp
Insert size: 162435; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality coverage: 4.5 in 020 bases; agarose-fp Quality coverage: 4.7 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                       1-164235
Birren B., Linton L., Nusbaum C., Lander E.;
"Homo sapiens chromosome 2, clone RP11-704A16";
"pubblished"
                                  09-APR-2000 (Rel. 63, Created)
14-MAY-2000 (Rel. 63, Last updated, Version 2)
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                    HTG; HTGS_DRAFT; HTGS_PHASE1.
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                                                                                                                                                                                         Homo sapiens (human)
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ACIO8072 AC036175
AC108072.2 GI:18376983
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...-. Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: submissions@watson.wustl.edu
Contact: Project Information
Center project name: H_NH0704A16
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Waterston, R.H.
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                          Db 95389 ATAATCTGGTCATGTTAA 95372
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                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 94.44
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
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       * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
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132885 164235; contig of 31401 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                              78456; gap of 100 bp
90502; contig of 12046 bp in length
90602; gap of 100 bp
110197; contig of 15595 bp in length
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                                                                                                                                                                                                                                                                                                                                          p of 100 bp contig of 10189 bp in length
                                                                                                                                                                                                                                                                                           p of 100 bp in length to of 100 bp in length to of 100 bp contig of 8298 bp in length
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10959: contig of 3849 bp in length
159: gap of 100 bp
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contig of 2304 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="2"
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39439; cont
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78356: cont
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58126: con
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                                                                                                          1307 1406; gap of 2680; cor
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                                                                                    1027 1126: gap of
1127 1306: co
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Submitted (24-JAN-2002) Genome Sequencing Center, Washington Submitted (24-JAN-2002) of Medicine, 4444 Forest Park Parkway, St. Louis, University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA On Jan 26, 2002 this sequence version replaced gi:18308946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166922 bp DNA linear HTG 26-JAN-2002 homospiens chromosome 2 clone RP11-704A16, WORKING DRAFT SEQUENCE, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
0; Caps
                                                                                                                                                                                                                                                                                                                                                                              Sequence 164235 BP; 52554 A; 29032 C; 29120 G; 51728 T; 1801 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.1%; Score 16.4; DB 30; Length 164235; 94.4%; Pred. No. 96; ative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
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Sequencing vector: plasmid; 57%
Sequencing vector: plasmid; 57%
Chemistry: Dye-primer Er; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 166298 bases at least Q40
Consensus quality: 166490 bases at least Q30
Consensus quality: 166729 bases at least Q30
Insert size: 168000; agarose-fp
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BETON OF SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Callo 18s, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestEsanger.ac.uk

On Sep 6, 2001 this sequence version replaced gi:14272282.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with a mall overlapping clone, as we submit sequences with This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI 05-SEP-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 176355)
Laird,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL356053 176355 bp DNA linear PRI 05-
Human DNA sequence from clone RP11-453G10 on chromosome 10,
                                                                                                           * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.1%; Score 16.4; DB 2; Length 166922; 94.4%; Pred. No. 96; Live 0; Mismatches 1; Indels 0;
Insert size: 166822; sum-of-contigs
Quality coverage: 11.20 in Q20 bases; agarose-fp
Quality coverage: 11.28 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                 1 1113: contig of 1113 bp in length 1213: gap of unknown length 4 166922: contig of 165709 bp in length. Location/Qualifiers 1. 166922
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/db_xref="taxon:9606"
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in the feature table with their source databases: Em:, EMBL; Sw:, SANISSPROT: Tr:, TREMBL; Wp:, WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contings of human chromosome 10, constructed by the Sanger Centre Chromosome 10 http://www.sanger.ac.uk/HGP/Chr10 RPI1-453G10 is from the library RPCI-11.2 constructed by the group http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RPI1-453G10 It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true right end of clone RPI1-453G10 is at 176355 in this sequence. The true right end of clone RPI1-19501 is at 100 in this
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Search completed: July 31, 2002, 14:02:35 Job time: 17597 sec

Thu Aug 1 08:30:06 2002

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:23:49; Search time 165.21 Seconds (without alignments) 35.683 Million cell updates/sec Run on:

1 tcagccagttccaccccgtgcacg US-09-899-718A-7 Perfect score: Sequence:

IDENTITY_NUC Gapox 1.0 Scoring table:

383533 seqs, 122816752 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%.
Maximum Match 100%
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	-09-060-756-461 Sequence 461 April	, α	2000000	seduence I,	-1 Sequence 3,	sequence I,	sequence 3	/oc acinembas	Jeduciice 1,	seduence 1,	US-08-581-1480-15	Sequence 13,	Socionos 1	'T adjusted 'T	· -	Sequence 1,	J Segmence	1	Segmence 8	April Des	7	ocuelibes:	Segment 1,	Sequence 1,	9-542B-29 Sequence 1,	2 Sequence 2	
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## ALIGNMENTS

Hour 1  10-060-756-461/c  10-060-756-461/c  10-060-756-461, Application US/09060756  10-060-756-461, Application US/09060756  10-060-756-461, Application US/09060756  10-060-756-461, Stewart  10-060-756-756-756-756-756-756-756-756-756-756	VEGANISM: Mycobacterium tuberculosis FERTURE: NAME/KEY: unsure LOCATION: (various positions within the sequence) OTHER INFORMATION: applicants are uncertain of bases designated as "n"	Score 17.6; DB 4; Length 114; Pred. No. 51; 0; Mismatches 4; Indels 0; Gaps 0 cg 24 ll cG 29
RESULT 1  US-09-060-756-461/c  Sequence 461, Application US/09060756  Patent No. 6183957  GENERAL INFORMATION:  APPLICANT: Cole, Stewart  APPLICANT: Gordon, Stephen  APPLICANT: Bilanlt, Alain  TITLE OF INVENTION: HERODE FOR ISOLATING  TITLE OF INVENTION: THE GENOME OF A MYCOB,  TITLE OF INVENTION: LIBRARY APPLICATION TF  FILE REFERENCE: 3495-0169  CURRENT APPLICATION NUMBER: US/09/060,756  CURRENT APPLICATION NUMBER: US/09/060,756  NUMBER OF SO ID NOS: 743  SOFTWARE: PATENTING DATE: 1998-04-16  NUMBER OF SO ID NOS: 743  SOFTWARE: PATENTING DATE: 1998-04-16  SEQUID NO 461  LENGTH: 114	; ORGANISM: Mycobacterium tuberculosis ; FEATUR: ; NAME/KEY: unsure ; LOCATION: (various positions within the sequence) ; OTHER INFORMATION: applicants are uncertain of ba US-09-060-756-461	Query Match 73.3%; Scor Best Local Similarity 83.3%; Pred Matches 20; Conservative 0; M Qy 1 toagcoagttccacccogtgcacg 24

RESULT 2
US-09-437-457-8/C
US-09-437-457-8/C
Sequence 8, Application US/09437457
Sequence 8, Application US/09437457
Sequence 8, Application US/09437457
Sequence 8, Application US/09437457
Sequence 9, Application Sequences and Methods For Sequences Applicant: Gardano, Anthony
TITLE OF INVENTION: INTERACTIONS AND METHODS FOR
TITLE OF INVENTION: INTERACTIONS AND MENA FUNCTIONALITY
TITLE OF INVENTION: INTERACTIONS AND MENA FUNCTIONALITY
FILE REFERENCE: 50093/01401
CURRENT APPLICATION NUMBER: US/09/437,457
CURRENT FILING DATE: 1999-11-10

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APPLICANT: Fagerstrom, Richard
APPLICANT: Aho, Sirpa
APPLICANT: Korhola, Mati
APPLICANT: Nevalainen, Helena
APPLICANT: Forhola, Mati
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                                                                                                                                                                                                             Query Match
71.7%; Score 17.2; DB 4; Length 230;
Best Local Similarity 86.4%; Pred. No. 75;
Matches 19; Conservative 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Ave., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0270004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
NUMBER OF SEQ ID NOS: 20 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/385,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08385370 Patent No. 5665585
                                                                                                                                                                                                                                                                                                                       2 cagccagttccacccgtgcac 23
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TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Cimbala, Michele A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1996 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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                                                                                                                  ORGANISM: Homo sapiens
US-09-437-457-8
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                                                                             LENGTH: 230
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                                                                                                       TYPE: DNA
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Gaps
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                                                                                                                                                                                                                                         APPLICANT: Variot, Aria
APPLICANT: Pagerstrom, Richard
APPLICANT: Regerstrom, Richard
APPLICANT: Aho, Sirpa
APPLICANT: Rorhola, Matti
APPLICANT: Norbala, Matti
APPLICANT: Norbalaine, Helena
TITLE OF INVENTION: Limit Dextrinase Activity in Trichoderma
NUMBER OF SEQUENCES: 7
CORRESPONDENCES: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/385,370
                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: Sterne, Kessler, Goldstein & Fox : 1100 New York Ave., Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0270004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/104,853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08303861
                                                                                                                      ; Sequence 3, Application US/08385370 ; Patent No. 5665585
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1473 TCCGCCAGCTCCACCCGGGCA 1494
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TELERA: (202) 371-2540
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                      APPLICANT: Torkkell, Tuula
APPLICANT: Joutsjoki, Vesa
APPLICANT: Torkkell, Helena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                    GENERAL INFORMATION:
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Query Match
Best Local Similarity 86.43
Matches 19; Conservative

Matches

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 21
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOCERSTER
STREET: 755 Page Mill Road
CITT: Pala Alto
STATE: California
COUNTRY: USA
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Fatent No. 6165461
GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATORIT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 cagccagttccaccccgtgc 21
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Washington
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; LOCATION: 97..
US-08-303-861-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT: Cole, Stewart
APPLICANT: Cole, Stewart
APPLICANT: Gordon, Stephen
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEGIIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE PEFEBENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/060,756
CURRENT FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: PALENTING OF MYCOBACTERIA
CONTAINS APPLICATION OF ALLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) LOCATION: (various positions within the sequence)
COTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-567
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O
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79.2%; Pred. No. 1.3e+02;
Live 0; Mismatches 5; Indels
                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: UA-APR-1998
                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUBER: 860098.421
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPAX: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4296 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 6183957
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  Floppy disk
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Best Local Similarity 90.09
Matches 18; Conservative
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Best Local Similarity 79.28
Matches 19; Conservative
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LOCATION: 193..3171
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MEDIUM TYPE:
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LENGTH: 374
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS FOR USE
                                                                                              APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USES
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107 FILING DATE: CONCURRENTY Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: Concurrently Herewith CLASSIFICATION 900
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-0CT-1992
FILING DATE: 02-0CT-1992
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA: 30-SEP-1993
APPLICATION NUMBER: US SN 08/422,560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US SN 08/422,560 FILING DATE: 14-APR-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                      Texas
: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08422560A
; Patent No. 5910626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 TTAGCCAGTTCCACCTCTAGCAC 365
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                                   Sequence 1, Application US/08611107
Patent No. 5801233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPAN: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, W
                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-08-611-107-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: Un
RESULT 8
US-08-611-107-1/C
                                                                                                                                                                                                                                                                                                                                        STATE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselkorn, Robert
APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE COMPOSITIONS AND
TITLE OF INVENTION: METHODS OF USE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patentIn Release #1.0, Version #1.30
                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/422,560A FILING DATE: 14-APR-1995 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA
APPLICATION NUMBER: US 08/422,560
FILING DATE: 14-APPL 1995
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                           ARCD: 152/WIM
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,700
FILING DATE: 02-007-1992
ATTORNEY/ACENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:152/W1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-418-3000
TELEFAX: 512-474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CITY: Houston STATE: Texas
COUNTRY: United States of America ZIP: 77210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRERY APPLICATION DATA:
APPLICATION NUMBER: US/08/468,793
FILING DATE: 06-JUN-1995
FILING DATE: 08-JUN-1995
FILING DATE: 08-JUN-1995
                                                                                                                                                IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 387 TTAGCCAGTTCCACCTCTAGCAC 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-468-793-1/c
; Sequence 1, Application US/08468793
; Patent No. 6177267
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tcagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 512-474-7577 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1458 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
STREET: P.O. Box 4433 CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                 FILING DATE: 14
CLASSIFICATION:
                                                                                      77210-4433
                                                                      USA
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                                                                                                                                                            COMPUTER:
                                                                      COUNTRY:
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/07903029
Fatent No. 596907
GENERAL INFORMATION:
APPLICANT: Wiegand, Roger C.
APPLICANT: Fok, Kam F.
TITLE OF INVENTION: Human Guanylin
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, Monsanto Co., A3SG
STREET: 800 M. Lindbergh Blvd.
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 0S/07/903,029
FILING DATE: 19920623
CLASSIFICATION: 530
ATTORNEY/AGENT INPORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/POCKET UNBER: 34,547
REEFERNCE/POCKET UNBER: 34,547
TELECOMMULCATION INFORMATION:
TELEPHONE: (314,694-5402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.5%; Score 16.2; DB 2;
85.7%; Pred. No. 1.9e+02;
tive 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                 266 TCAGCCGGTACCACTCCTTGCAC 288
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; Patent No. 6162908
                                                                                                                                                                                                                                                                      1 tcagccagttccaccccgtgcac 23
               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 TCACCCAGTTCCTCCCGGGC 480
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TELEPAX: (314)694-9009
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            Query Match 69.28
Best Local Similarity 82.68
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 589 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.78
Matches 18; Conservative
                                                                                                   1..1665
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US-07-903-029-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                             ; NAME/KEY: CDS
; LOCATION: 1..1
US-08-581-148C-15
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US-07-903-029-2/C
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US-09-155-768-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schable, Patrick S.
APPLICANT: Robertson, Donald S.
APPLICANT: Hansen, Joel D.
APPLICANT: Nikolau, Basil J.
APPLICANT: Xia, Xiaojie
APPLICANT: Xia, Xiji
TITLE OF INVENTION: ISOLATION AND USE OF CUTICULAR LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MA-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/581,148C
FILING DATE: 29-DEC-1995
CLASSIFICATION: 800
                                                CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: 33,928
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELEPHONE: (512) 418-3000
TELERX: 79-0924
INPORMATION FOR EXQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 1458 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
             APPLICATION NUMBER: PCT/US93/09340 FILING DATE: 30-SEP-1993 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Larcher, Carol
REGISTRATION NUMBER: 35243
REPRENCE/DOCKET NUMBER: 71380
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 616-5600
TELEFAX: (312) 616-5700
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                             . INVECTORY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08581148C Patent No. 6060644 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcagccagttccaccccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1903 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 60601-6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-581-148C-15
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Gaps

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APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                 SEO ID NO 1
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APPLICANT: WHITE, OWEN R.

APPLICANT: WENSER, Claire M.

APPLICANT: PERSER, Claire M.

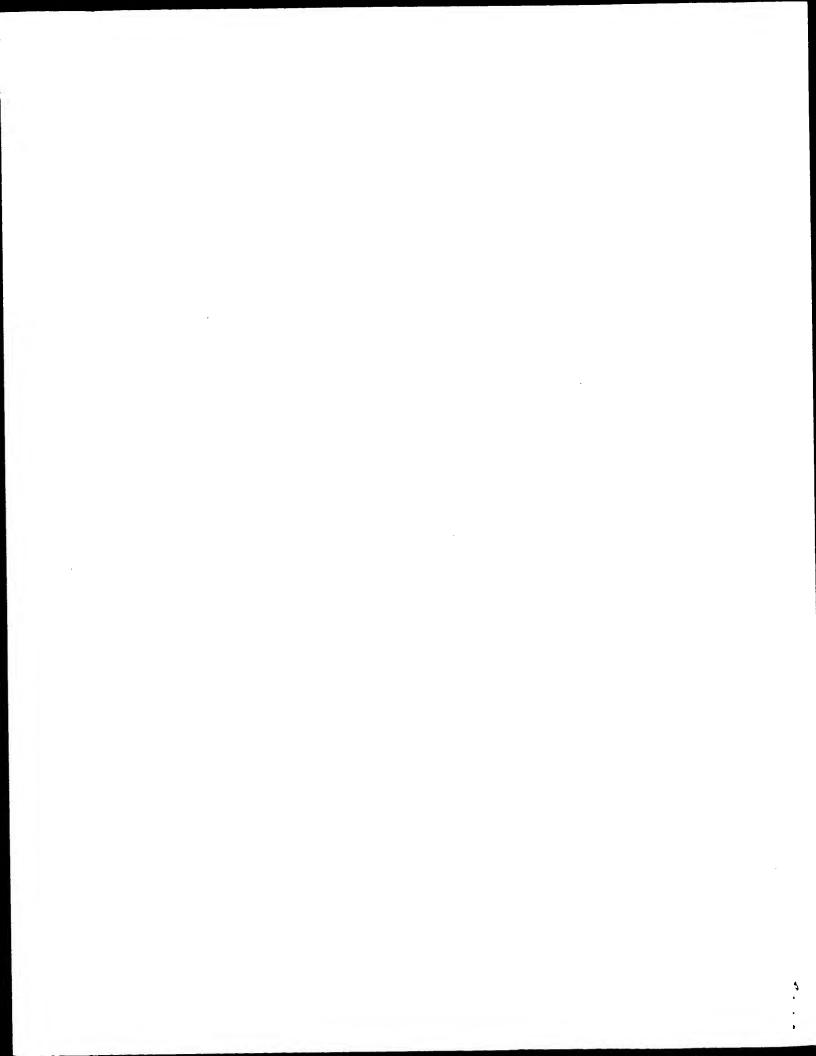
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT PEPLICA DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOSTWARE: PATENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.5%; Score 16.2; DB 4; Length 4403765; Best Local Similarity 90.0%; Pred. No. 54; Matches 18; Conservative 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 67.5%; Score 16.2; DB 4; Length 2117; Best Local Similarity 85.7%; Pred. No. 1.9e+02; Matches 18; Conservative 0; Mismatches 3; Indels 0;
                                                   AFFLICANT: BALFACHEN CONCURS. CONTROLL OF HYALURONAM SYNTHASE OF TITLE OF INVENTION: POLYPEPTIDE OF HYALURONAM SYNTHASE OF TITLE OF INVENTION: HUMAN-ORIGIN AND DNA ENCODING THE SAME FILE REFERENCE: TOYAM37.001APC
CURRENT APPLICATION NUMBER: US/09/155,768A
CURRENT PELLOR DATE: 1996-10-05
EARLIER PELLING DATE: 1996-04-05
EARLIER PLILING DATE: 1996-04-30
NUMBER OF SEQ ID NOS: 4
SOFWARE: FRSELEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 2098669 CACCCAGTTCCACCGGGTGC 2098650
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1374 GCCAGTGCCACGCCTGCACG 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 gecagttecacecegtgeacg 24
                      GENERAL INFORMATION:
APPLICANT: SEIKAGAKU CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 cagccagttccaccccgtgc 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (149)...(1777)
US-09-155-768-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4403765
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US-09-103-840A-1/C
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-103-840A-2/c
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 1
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OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:09; Search time 5855.71 Seconds (Without alignments) 55.318 Million cell updates/sec Run on:

US-09-899-718A-7 24 1 tcagccagttccacccgtgcacg 24

Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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## ALIGNMENTS

GALVA193  GA_EB0023J06f Gossypium arboreum 7-10 dpa fiber library Gossyplum arboreum arboreum 7-10 dpa fiber library Gossyplum B6444193  EG444193.1 GI:13353845  EG5444193.1 GI:13353845  EST.  Gossypium arboreum.  Gossypium arboreum.  Gossyplum arboreum.  Ming, R.A., Frisch,D., Yu.Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leeslie,A. and Wilkins,T.A.  Ming, R.A., Frisch,D., Yu.Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leeslie,A. and Wilkins,T.A.  Ming, R.A., Frisch,D., Yu.Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leeslie,A. and Wilkins,T.A.  Gossyplum arboreum.  Gossyplum arboreum.  Gossyplum arboreum.  Contact: Wing RA  Clemson University  Tel: 864 656 728  Fax: 864 656 728  Email: rwing@clemson.edu  Seq primer: TAATACGACTCACTATAGGG  High quality sequence stori: 2  High quality sequence stori: 3  1. 836  // Organism="Gossyplum arboreum"  // Strain="MAR"  // Organism="Gossyplum arboreum"  // Strain="MAR"  // Organism="Gossyplum"  // Observation-19729"	/ub_xrer="axon:39/29" /clone="GA_2003306f" /clone=llb="Gossypium arboreum 7-10 dpa fiber library" /tissue_type="Fibers isolated from bolls harvested 7-10 dpa" /lab_host="E. coli"
RESULT 1 BG444193/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL COMMENT SOURCE	

Query Match

Matches

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BASE COUNT

DEFINITION

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ORGANISM

AUTHORS

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Fax: 81-298-38-7468
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roset-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Roset-Crollius, H., Jaillon, O., Brottler, P., Quetier, F., Barnot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F., Saurin, W. and Weissenbach, J. ..., Saurin, W. and Weissenbach, J. ..., Saurin, W.
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Query Match

Matches

RESULT

BASE COUNT

ORIGIN

TITLE JOURNAL

COMMENT

FEATURES

JOURNAL AUTHORS

TITLE

REFERENCE

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AUG65405
AUG65405 Rice root Oryza sativa cDNA clone R3592_lA, mRNA sequence.
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1 (bases 1 to 453)
Minobe, Y. and Sasaki, T.
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420 bp mRNA linear EST 24-OCT-1996 C19505 Rice panicle at ripening stage Oryza sativa cDNA clone E10225.1A, mRNA sequence.
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
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Contact: Takuli Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                Fice cDNA from panicle at ripening stage Unpublished (1996) Contact: Takuji Sasaki Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
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REFERENCE
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                                                                                                                                                                                                                                                                                                                  AU065404 AU065404 Rice root Oryza sativa cDNA clone R3590_1A, mRNA sequence. AU065404
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BB170026B10G05 Bee Brain Normalized/Subtracted Library, BB17 Apis
mellifera cDNA clone BB170026B10G05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 460)
Minobe, Y. and Sasaki, T.
Rice CDNA from root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1995)
Contact: Takuji Saski
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 81-298-7441
Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                 Gaps
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                                                                                                                                         Score 18.8; DB 9; Length 453;
Pred. No. 1.3e+03;
0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18.8; DB 9; Length 460; Pred. No. 1.3e+03;
/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
                     /clone="R5592_lA"
/clone=lib="Rice root"
/note="Prepared from seedling root."
/note="Prepared from seedling root."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="Nipponbare, sub_species Japonica"
/dxxref="taxon:4530"
/clone="R3590_lA"
/clone="Rice root"
/note="Prepared from seedling root."
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BI510068.1 GI:15360442
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90.9%;
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90.9%;
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Best Local Similarity 90.99
Matches 20, Conservative
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505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: generobielife.uiuc.edu
This research was funded by the University of Illinois Critical
Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
Award in Functional Genomics to G.E. Robinson and an NSF
Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
                       Anote—"Organ: brain; Vector: pT7T3-Pac; Site_1: EcoR1; Site_2: Not1; This BB17 cDNA library was generated by subtraction of the BB16 library with 4000 previously sequenced clones. The BB16 library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of various ages and various behavioral groups. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Apis mellifera"
/strain=mixed strains of European bees, predominantly
A.m. ligustica "
/db_xref="taxon:7460"
/clone="BB170026810G05"
/clone=lib="Bee Brain Normalized/Subtracted Library, BB17"
/sex="female"
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 426)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Pred. No. 2.2e+03;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: ATTAACCCTCACTAAAG
Insert Length: 306 Std Error: 0.00
Plate: BB170026B10 row: G column: 0
Seq primer: AGCGGATAACAATTTCACACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 306.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORWARD: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                         Contact: Gene E. Robinson
Department of Entomology
University of Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 TCGCCAGTTCCACCGCGTGCTC 278
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87.0%;
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Matches 20; Conservative
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AUTHORS

JOURNAL MEDLINE

COMMENT

TITLE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 559) Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casaa, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 02-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK; Site_1: Sal1; Site_2: Not1; Cambial region tissues, including developing xylem, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    meristematic cambial zone and the developing and mature phloem, was harvested from 1.5 m actively growing trees. CDNA was prepared and cloned into lambda g122a. DNA was isolated and subcloned into pBluescript SK using SalI and NoII restriction enzymes. 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Design and use of two pooled tissue normalized CDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Populus tremula x Populus tremuloides"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.8%; Score 18.2; DB 9; Length 528; 87.0%; Pred. No. 2.3e+03; tive 0; Mismatches 3; Indels (
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239242 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Hybrid aspen plasmid library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
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Fax: 402 762 4390
Contact: Sterky F
Department of Biotechnology
Royal Institute of Technology (KTH)
Teknikringen 34, S-100 44 STOCKHOLM, Sweden
Tel: +46 8 790 8287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, U
                                                                                                                                                                                                                           FORWARD: AAAGGGGATGTGCTGCAAGGCG
BACKWARD: GCTTCCGCTCGTATGTTGTGTG
Seq primer: CGTTGTAAAACGACGCCAG
High quality sequence stop: 528.
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Plate: 67 row: B column: 7
Seg primer: ATTTAGGTGACATATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:47664"
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                                                                                                                                                                          fredrik@biochem.kth.se
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                                                                                                                                                Fax: +46 8 24 54 52
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Gene discovery in the wood-forming tissues of poplar: Analysis of 5,692 expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 95 (22), 13330-13335 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: colon_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES POR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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                                        Dias Neto, E., García Correa, R., Verjovskí Almeida, S., Elloues, P. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Nagai, M. A., de Carvalho, R.F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deolivelar, P. S., Bucher, P., Jongeneel, C. V., O' Hare, M. J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S. J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-CN0089-070201-746=e01&t3=2001-02-07&t4=1)
Seq primer: puc 18 forward
                       Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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/dev_stage="Adult"
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136 TCAGCCAGCTCCACCGGGTGCAC 114
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/db.xref="taxon:9606"
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Site_2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: gGCACGGGG(0: Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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687 bp mRNA linear EST 22-MAY-2001

602748468BI NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4901416 5',
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NIH-MGC http://mgc.nci.nih.gov/.
                                                                                               /note="Vector: pCMV SPORT6; Site_1: xbai; Site_2: xhoi; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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High quality sequence start: 4
High quality sequence stop: 551.
Location/Qualifiers
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                   /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
/organism="Sus scrofa"
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/lab_host="DH10B"
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/organism="Homo sapiens"
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                                                                     /clone="IMAGE:4422900"
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                                                                                                                                                                                                                                                                                 Email: szhaoétigr.org

Email: szhaoétigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Clones are derived from the mouse BAC library availablity, please contact Pieter de Jong

library availablity, please contact Pieter de Jong

(pdejongemail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html

Seq primer: 77
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov plate: LLCMISIS row: e column: 13
High quality sequence stop: 710.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: APCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                       Oppublished (1999)
Other GSSs: RPCI-24-301P3.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for
      Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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/cell_type="Spleen/Brain"
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/organism="Mus musculus"
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/clone="RPCI-24-301P3"
/clone_lib="RPCI-24"
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/clone_lib="NIH_MGC_20"
/clone_lib="NIH_MGC_20"
/tissue_type="melanotic melanoma" .
/tissue_liblus (phage-resistat) .
/tistue_long niskin; Vector: poTBF; Site_1: XhoI; Site_2:
/cloned into EcoRI/XhoI sites using the following 5
/cloned into EcoRI/XhoI sites using the following 5
/cloned into EcoRI/XhoI sites using the following 5
/cloned into EcoRI/XhoI sites susing the following 5
/cloned into EcoRI/XhoI sites susing the following in insert size 1: 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Carlifornia, Berkeley) using zAP-cDNA synthesis kit (Stratagane) and Superscript II RT (Life Technologies).
// 46 a 275 c 339 g 147 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus adult male tongue cDNA, RIKEN full-length enriched
library, clone:2300002M23:hypothetical protein, full insert
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="tongue"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. 1200
/note="evidence:NAS
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/db_xref="MGD:MGI:1901684"

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    /organism="Mus musculus"

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/clone="2300002M23"
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(http://www.jax.org/missources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymuclectide kinase. Adaptor oligonuclectides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321141gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                   Mus musculus Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 64)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Kose, M., Rose, M., Rose, M., Stokes, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0190 row: G column: 02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plate: 0190 row: G column: 02
Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                     plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 64.
Location/Qualifiers
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/clone="UUGC2M0190G02"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
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Fax: 801 585 7177
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house mouse.
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Best Local Similarity
Matches 19; Conserve
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Page 8

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 31, 2002, 14:11:24; Search time 720.8 Seconds (without alignments) 57.167 Million cell updates/sec Run on:

US-09-899-718A-7

1 tcagccagttccacccgtgcacg 24 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1736436 seqs, 858457221 residues Searched:

3472872 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

N_Geneseq_032802:*	1: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT: 2: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981_DAT:	` `	4: /SIDS1/gcgdata/hold-geneseg/genesegn-emb1/NA1983.DAT:	5: /SIDS1/gcgdata/hold-geneseg/geneseqn-embl/NA1984.DAT:	6: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:	7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:	8: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1987.DAT:	9: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1988.DAT:	10: /SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1989.DAT:	11: /SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1990.DAT:	12: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:	13: /SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1992.DAT:	14: /SIDS1/gcgdata/hold-geneseq/genesegn-embl/NA1993.DAT:	15: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1994.DAT:	16: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:	17: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:	18: /SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA1997.DAT:	19: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1998.DAT:	20: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:	21: /SIDS1/gcgdata/hold-geneseq/genesegn-embl/NA2000.DAT:	22: /SIDS1/gcgdata/hold-geneseg/genesegn-emb1/NA2001A.DAT:	23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT:	24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Score Match Length DB III 18.2 75.8 7555 11 7 17.6 73.3 555 15 7 17.2 71.7 657 15 7 17.2 71.7 657 15 7 17.2 71.7 657 15 7 17.2 71.7 1965 24 7 17.2 71.7 1972 23 7 17.2 71.7 1972 23 7 17.2 71.7 1972 23 7 17.2 71.7 1972 23 7		Description		. Cardiac sodium cha								cDNA encoding gluc
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PD	23-AUG	JG-1	-1990.								
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XX PI	Rogart		RB;								
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XY	New rat c	rat	σ,	liac	sodi	um cl	channel.	ins - and associate	associated d with	DNA	
I. I.	proteins,	eins		efu	useful as ant	anti	arryt	antiarrythmic and cardiotonic	nic drugs.		

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Sequence 7555 BP; 1577 A; 2309 C; 2103 G; 1566 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tcagccagttccaccccgtgcacg 24
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                                                                                                                                        1 tcagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL24072 standard; DNA; 4541 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (COMM-) COMMON SERVICES AGENCY.
                                                                                                                                                                                                                                                                             AAQ73770 standard; cDNA; 57 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MURE-) MUREX DIAGNOSTICS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94GB-0000263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-GB00957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93GB-0009237.
                                                                                                                                                                                                                                                                                                                                                          26-MAY-1995 (first entry)
                                                                              Best_Local Similarity 87.09
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pike IH, Simmonds P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-358278/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9425602-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1994.
                                                                                                                                                                                                                                                                                                                      AAQ73770;
                                                            Query Match
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                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sodium channel protein; ds; therapeutic; diagnostic; prognostic; antiarrythmic; cardiant; cardioglycoside; pRH3-1; pRH4-23; pRH14-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The cDNA is derived from 3 overlapping cDNA clones, designated plasmid pRH4-23 (ATCC 67885), plasmid pRH4-23 (ATCC 67885) and plasmid pRH4-131 (ATCC 67887). A virus/circular DNA plasmid vector comprising the cDNA may be transformed or transfected into a
                                 The sequence is derived from 3 overlapping clones, pRH3-1,pRH4-23, and pRH4-31. (Deposited as ATCC 67885, 67886, and 67887 resp.) The clones were isolated from a cDNa library in the lambda Zap vector prepd. from mRNA obtd. from newborn rat hearts using rat brain II cDNA probe. The isolated DNA can be used to screen a
                                                                                                                                      human derived cardiac cDNA library for the corresponding one. Proteins produced by expression of the DNA have
                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                           Score 18.2; DB 11; Length 7555; Pred. No. 1.2e+02; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Purified DNA's encoding rat and human cardiac sodium channel protein - useful for recombinant expression to produce sodium
                                                                                                                                                                                                                   Sequence 7555 BP; 1576 A; 2314 C; 2101 G; 1564 T; 0 other;
                                                                                                                                                                              diagnostic therapeutic, and prognostic applications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cardiac sodium channel protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Fig la-1n; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                539 tcagccccttccaccccgtgcgc 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAQ81328 standard; cDNA; 7555 BP.
                                                                                                                                                                                                                                                                                                                                                            1 tcagccagttccaccccgtgcac 23
Claim 7; Fig 1; 65pp; English.
                                                                                                                                                                                                                                                                               75.8%;
87.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARCH-) ARCH DEV CORP.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1991;
                                                                                                                                                           human gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ81328;
                                                                                                                                        similar
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                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HCV-4; HCV-5; HCV-6; NS4; NS5; non-structural protein; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; vaccine; diagnosis; therapy; typing; immunoassay; ss.
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0
75.8%; Score 18.2; DB 16; Length 7555; 87.0%; Pred. No. 1.2e+02; Live 0; Mismatches 3; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral RNA from HCV-infected patients was subjected to PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57 BP; 14 A; 16 C; 13 G; 14 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis C virus type-specific sequence.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Untranslated region; UTR; RNA binding protein; RBP; neurodegeneration; stroke; cardiovascular disease; hypertension; cancer; inflammation; metabolic disorder; obesity; diabetes; beta-2 adrenergic receptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human beta-2 adrenergic receptor UTR region with RBP binding ability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 17.4; DB 23; Length 4541;
Pred. No. 2.7e+02;
0; Mismatches 1; Indels 0;
                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 23689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 23689; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4541 BP; 1232 A; 1097 C; 1013 G; 1199 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH27139 standard; DNA; 230 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 72.5%;
Local Similarity 94.7%;
nes 18; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 agccagttccacccgtgc 21
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11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US09231
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                                            26-MAR-2002 (first entry)
                                                                                                                                                           pharmaceutical; gene; ds
                                                                                                                                                                                                      Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                 WO200171042-A2.
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    ABL24072;
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Matches
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Sequences AAH27132 - AAH27151 represent human gene untranslated regions where the corresponding mRNA fragment has RNA binding protein (RBP) binding activity RBPs mediate the processing of pre-mRNA, the transport of mRNA from the nucleus to the cytoplasm, mRNA stabilisation. translational efficiency, and the sequestration of some mRNAs. Therefore modification of post-transcriptional protein expression in eukaryotic cells may be carried out through the targeting specific interactions of proteins that bind to RBPs. The gene fragments of the invention are used to identify their optimized sub-fragments, compounds that affect RNA/RBP interaction or mRNA functionality; or RBPs that interact with the compounds. Compounds identified using the gene fragments are potentially useful for therapeutic regulation of gene expression, such as in cases of neurodegeneration; metabolic disorders (obesity and diabetes) and bacterial or infilanmaths of the compounds of the content of the compounds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        viral infection. The present sequence is one of gene fragments of the invention, isolated from the human beta-2 adrenergic receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acids that bind RNA-binding proteins or regulate mRNA function, useful for therapeutic gene regulation, such as in cases of neurodegeneration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 230 BP; 42 A; 91 C; 70 G; 27 T; 0 other;
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/product= rat_proteosome_RING12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ54681/c
ID AAQ54681 standard; cDNA to mRNA; 657 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 28; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 caqccaqttccacccqtqcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 CTGCCAGTTCCAGCCCGTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92JP-0154184.
                                                                                                                                     99US-0437458
                                                                    09-NOV-2000; 2000WO-US30888
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                                                                                                                                                                                                         (MESS-) MESSAGE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                                                                                                                             Giordano A, Xavier AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .657
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                                                                                                                                     10-NOV-1999;
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17-MAY-2001.
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Best Local Similarity 86.48 Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
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                      MPL activity -
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                                                                                                                                                         in AAU09495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide polymorphisms in the human myeloproliferative leukemia virus
                                                                                                                                                                                                                                                                                                                                                                    myeloproliferative leukaemia virus oncogene; haplotyping; genotyping; congenital amegakaryocytic thrombocytopaenia; CAMT; ds.
                                                                                                                                                                                                           Gaps
                                                                                                               Sequences (AAQS4678-81) show various components of a rat proteosome. The component is useful for the elucidation of various mechanisms of diseases such as malignant tumours and their diagnosis and
                                                                                                                                                                                                                                                                                                                                                           Human; single nucleotide polymorphism; SNP; MPL; chromosome 1p34;
                                                                     A component of rat proteosome - for elucidation of mechanism of
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0
                                                                                                                                                                                      Query Match 71.7%; Score 17.2; DB 15; Length 657; Best Local Similarity 86.4%; Pred. No. 2.9e+02;
                                                                                                                                                                                                         3; Indels
                                                                                                                                                           Sequence 657 BP; 137 A; 184 C; 198 G; 138 T; 0 other;
                                                                                                                                                                                                                                                                                                                                          Reference sequence for human MPL gene exons 9-10.
                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chew A, Choi JY, Koshy B, Stephens JC;
                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                         (BIOM-) BIO MATERIAL KENKYUSHO KK.
                                                                                              Claim 8; Page 5-6; 24pp; Japanese.
                                                                                                                                                                                                                                   275 TCCTCCAGTTCCAACCCGTGCA 254
                                                                                                                                                                                                                                                                                      AAS19511 standard; DNA; 1785 BP.
                                                                                                                                                                                                                         1 tcagccagttccaccccgtgca 22
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        92JP-0154184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2001; 2001WO-US12301.
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1028..1124
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                                                                                                                                                                                                         19; Conservative
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                                                                             e.g. malignant tumour
                                           WPI; 1994-011024/02.
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                                                     P-PSDB; AAR47473
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       22-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                                            creatment.
                                                                                                                                                                                                                                                                                                        AAS19511;
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oncogene (MPL) gene, useful for studying the function of and expressing MPL protein for use in screening drugs for treating diseases related to {\sf total}
                                                                                                                                                                                                                                                           The present invention relates to novel single nucleotide polymorphisms (SNPs) in the human myeloproliferative leukaemia virus oncogene (MPL) gene located on chromosome lp34, and methods for haplotyping and/or genotyping the MPL gene. The methods of the invention make use of allele-specific oligonucleotides (ASOs) as probes and primers and/or primer-extension oligonucleotides for detecting MDL gene polymorphisms. The polymucleotides and screened compounds are useful for the treatment of diseases associated with MPL activity, such as congenital amegakaryocytic thromborytopaenia (CAMT). The present sequence represents a reference sequence for human MPL gene exons 9-10. Note: This sequence encodes for only part of the MPL protein shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #27614.
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                                                                                                                                                                                     Claim 27; Fig 3; 85pp; English.
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in chaptonstics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amno acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glucoamylase P; hormoconis resinae; debranching activity; enzyme; dextrinase activity; Trichoderma reesei; starch granule; preservation; hydrolysis; gelatinised starch; glucose syrup; straight linear dextrin; saccharification; lignocellulosic material; sugar utilisation;
                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                             Score 17.2; DB 23; Length 1972;
Pred. No. 3.1e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nevalainen
                                                                                                                                                                                                                                                                                               Sequence 1972 BP; 460 A; 523 C; 552 G; 437 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Korhola M,
                                                                                                                                                                                                                                                 specification, but was obtained in electroni
at ftp.wipo.int/pub/published_pct_sequences.
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Vainio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT90830 standard; cDNA; 1996 BP
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0
                                                                                                                                                                                                                                                                                                                                                                                                                              2 cagccagttccacccgtgcac 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA encoding glucoamylase P.
                                                                                                                                                                                                                                                                                                                                                71.78;
86.48;
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2515..2520
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 86.47
Matches 19; Conservative
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Torkkeli H, Torkkeli T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           feed additive; ss.
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beta2 adrenergic receptor; genetic variation identification; hypertrophy; disease diagnosis; hypertension; prostatic disease; pulmonary disorder; asthma; peripheral vascular disorder; neuropsychic disorder;
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                                                                                                                                                                                                                                                            Score 17.2; DB 18; Length 1996; Pred. No. 3.1e+02; 0; Mismatches 3; Indels 0;
                                  AAT90830 and AAT90831 represent the cDNA and gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                 AlphalB-adrenergic receptor; human; cardiovascular disease;
                                                                                                                                                                                                                                     Sequence 1996 BP; 474 A; 574 C; 491 G; 457 T; 0 other;
Trichoderma to produce recombinant glucoamylase P
                                                                                                                                                                                                                                                                                                                                                                                                                 Human beta2-adrenergic receptor gene.
                 Claim 2; Column 55-58; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endocrine-metabolic disorder; ss.
                                                                                                                                                                                                                                                                                                          1473 tccgccagctccaccccgggca 1494
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86.48;
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Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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temperature 50.85 deg. C. Bach pair of primers is: non-cross-hybridising, commends to two distinct segments (separated by at least 400 nt); and generature 50.85 deg. C. Bach pair of primers is: non-cross-hybridising, anneals to two distinct segments (separated by at least 400 nt); and generates a homogeneous population of gene segments in a polymerase chain reaction (PCR). At least one primer in the pair can extend a 3'-end sequence complementary to a template sequence in a DNA polymerase chain sequence complementary to a template sequence in a DNA polymerase craction. The primers are used to amplify segments of the alphalB and beta2 adrenergic receptor genes, particularly to identify genetic variations for diagnosis of disease. Specifically variations in the beta2 darenergic receptor genes, particularly to identify genetic cardiovascular disease (hypertrophy), and those in the beta2 gene with cardiovascular disease, hypertension and asthma, but variations may also be associated with peripheral vascular, pulmonary, neuropsychic and endocrine-metabolic disorders. These primers allow rapid and specific amplification of large and homogeneous gene segments of the alphalB and beta2 genes firm a complex mixture of DNAS. This makes possible detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is amplified by the primers of the invention. The primers are non-self hybridising; contain at least 15 nucleotides (nt) and has a melting
                                                                                                                          This sequence represents the human beta2-adrenergic receptor gene, and
Disclosure; Fig 2; 58pp; English.
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Sequence 2300 BP; 495 A; 613 C; 646 G; 546 T; 0 other;

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Gaps
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     71.7%: Score 17.2; DB 20; Length 2300; 86.4%; Pred. No. 3.1e+02; Live 0; Mismatches 3; Indels 0;
                                                                            616 CTGCCAGTTCCAGCCCGTGCTC 595
                                                            2 cagccagttccacccgtgcac 23
Query Match
Best Local Similarity 86.48
                                                            δλ
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polymorphism; polymorphic marker; cardiovascular disease; myocardial infarction; unstable angina; hypertension; atherosclerosis; stroke; prognosis; drug screening; treatment outcome; human; ds.
                                                                                                                                                                                                                                                                                        Andersson MK, Lindstrom PHR, Jonsson L;
                                                                                            Beta-adrenergic receptor-2 gene; coding region;
                                                                       Human beta-adrenergic receptor-2 coding region.
          AAA38340 standard; DNA; 2305 BP.
                                                                                                                                                                                                                                               98US-0104302.
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                                                   21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                   (EURO-) EURONA MEDICAL AB.
                                                                                                                                                                                                                                                                                                            WPI; 2000-318010/27.
                                                                                                                                                                    WO200022166-A2.
                                                                                                                                                                                                               13-OCT-1999;
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                                                                                                                                                                                          20-APR-2000.
                               AAA38340;
AAA38340/
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Assessing cardiovascular status in humans involves comparing test polymorphic pattern comprising polymorphic positions within genes encoding specific proteins, with reference polymorphic pattern

Disclosure; Page 124-125; 126pp; English.

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cardiovascular disorders such as myocardial infarction, unstable angina, hypertension, atherosclerosis and stroke. They are also useful for predicting the likely cardiovascular status of a patient given a creatment regimen comprising administration of cardiovascular drugs confiders to be cardiovascular cardiovascular drugs (e.g., ACE inhibitors, beta-adrenergic receptor antagonists (beta-blockers) one or more polymorphic markers browides a basis for predicting the outcome of a treatment regimen. Fragments of the genes comprising a polymorphic site may be used as primers and probes for detecting genetic polymorphisms or in molecular creaments of the genes comprising a polymorphic pattern reduces or they encode are useful in the screening of potential cardiovascular crucks. Determination of an individual's polymorphic pattern reduces or individual cardiovascular patient. It also provides the ability to climinate patients from chinical trials who are predicted to be non-responsive, or at a risk for an adverse response, to a particular cardiment regimen. Adverse results in an early trial can be evaluated to identify polymorphic patterns so that the adverse results can be evaluated correlated with a sub-population of the test population, permitting decreasing the number of patients required for a patricital population in the proportiate population, therefore the interest of patients required for a patients required the interest of the number of patients required for a patients required the interest of the patients required for a patients required the interest of the patients required for a patient of the patients required for a patient required the interest of patients required for a patients required in the number of patients required for a patient of the patients required for a patient required the patient of the patients required for a patient which is the patients required the patients required fo
The invention relates to a novel method of assessing the cardiovascular status in an individual and to newly identified polymorphisms in the genes encoding angiotensin-converting energyme (ACE), angiotensin II receptor type 1 (ATI) and type 2 (ATI), angiotensinogen (ACT), renin, aldosterone synthase, endothelin receptor type A and beta-adrenergic receptors I and 2. The method comparises determining the sequence at one or more polymorphic positions within these genes, and comparing the pattern of polymorphisms from the individual with a reference polymorphic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  decreasing the number of patients required for a clinical trial, which in turn decreases the duration and cost of such trials. The present sequence represents the human beta-adrenergic receptor-2 gene
                                                                                                                                                                                                                                                     pattern obtained from a population of individuals exhibiting a predetermined cardiovascular disease status. The polymorphic markers are useful for determining the predisposition of an individual to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding region (GenBank Y00106/g293708). The polymorphic sites identified are 839A/G, 872C/G, 1045A/G, 1284C/T, 1316A/C, 1846C/G, 2032A/G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 17.2; DB 21; Length 2305; 86.4%; Pred. No. 3.1e+02;
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AAA38784/c
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Hormoconis resinae.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glucoamylase P; hormoconis resinae; debranching activity; enzyme; dextrinase activity; Trichoderma reesei; starch granule; preservation; hydrolysis; gelatinised starch; glucose syrup; straight linear dextrin; saccharification; lignocellulosic material; sugar utilisation; feed additive; ss.
                                                                                                                                                                                                                                                                                                                                                              Polymorphisms in the leader cistron (LC) of the beta 2-adrenergic receptor (beta 2 AR), useful for predicting genetic disposition to a disease modified by beta 2 AR expression e.g. congestive heart failure,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
'note= "no stop codon given at 3' end of sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2340 BP; 498 A; 627 C; 653 G; 562 T; 0 other;
                                            /*tag= b
/label= 5'_leader_cistron
replace(1541,T)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Figure 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1410 CTGCCAGTTCCAGCCCGTGCTC 1389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT90831 standard; cDNA; 2745 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determine the best treatment.
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1588..2340
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              /partial
1487. 154
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                  WPI; 2000-400107/34.
                                                                                                                                                     WO200031307-A1
                                                                                                                                                                                                                                                                                                                                                                                                                nypertension
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                                                                                                                                                                                                               24-NOV-1999;
                                                                                                                                                                                                                                           25-NOV-1998;
                               sig_peptide
                                                                                                         nat_peptide
                                                                                                                                                                                   02-JUN-2000
                                                                                                                                                                                                                                                                                                         Liggett SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT90831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Hormoconis resinae glucoamylase P, respectively. These sequences are used in the composition of the invention and are capable of being processed by a Trichoderma host cell. H. resinae glucoamylase P has higher debranching and dextrinase activity than conventional glucoamylase-pullulanase mixtures. T. reesel secretes enzymes that are important for the degradation of complexes around and in starch granules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormoconis resinae glucoamylase P gene construct - for transforming Trichoderma to produce recombinant glucoamylase P \,
                                                                                                                                                                                                                                                 /number= 1
/note= "designated IVS (intervening sequence) 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "designated IVS (intervening sequence) 3"
1637..2447
                                                                                                                                                                                                                                                                                                                                                                                                                   nnote= "designated IVS (intervening sequence) 2" [075..1583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Korhola M, Nevalainen H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT90830 and AAT90831 represent the cDNA and gene encoding the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "encodes residues 178 to 347"
[584..1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "encodes residues 348 to 616"
2448..2745
                                                                                                                                                                                                                                                                                                                      /number= 2
/note= "encodes residues 76 to 177"
                                                                                                                                                                        /number= 1
/note= "encodes residues 1 to 75"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Joutsjoki V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 2; Column 60-66; 61pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vainio A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0104853.
92US-0937789.
95US-0385370.
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2515..2520
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295..520
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                                                                                                                                                                                                                                                                                                                                                              ..1074
                                                                                            25. 229
                                                                                                                                                                                                           .593
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                                                                                                                                                                                                                                                                                  594..898
                                       /*tag=
87..90
/*tag=
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                     . 294
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P-PSDB; AAW30155.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-1992;
07-FEB-1995;
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                                                                                                TATA_signal
                                                           CAAT_signal
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starch or the presence of a debranching activity. These applications starch or the presence of a debranching activity. These applications starch or the presence of a debranching activity. These applications include starch analysis, the manufacture of glucose syrups, production of straight linear dextrin for use in food, medicines and cosmetics, and in the preparation of food fibers by the enzymatic treatment of seed husks or brans. The enzyme can also be used as an additive to laundry and dish washing detergents, in wood and textile industry applications such as the preparation of plywood and textile industry applications such as saccharification of plywood adheaves. It can also be used in the saccharification of lignocellulosic materials, the preparation of feedstuff from meat by products and to improve utilisation of sugar present in such feedstuff. When used as a feed additive for food animals, the recombinant bacterial biomass may be added directly to the
The recombinant glucoamylase P enzyme produced by the Trichoderma host
                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reactions upon regular administration - by identifying patients homozygous for allele encoding Arg at position 16 of
                                                                                                                                                                                                                                                                                                                                                                  71.7%; Score 17.2; DB 18; Length 2745; 86.4%; Pred. No. 3.1e+02; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing asthma patients predisposed to adverse beta-agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= b
/note= "A to G substitution, results in Arg16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boushey H, Chinchilli VM, Drazen JM, Fish JE, Ford JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-2-adrenergic receptor; human; asthma; beta-agonist;
                                                                                                                                                                                                                                                                                                          Sequence 2745 BP; 643 A; 760 C; 667 G; 675 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to Gly amino acid change"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human beta-2-adrenergic receptor cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           beta2-adrenergic receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAV52614 standard; cDNA; 3451 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2040 tecgeeagetecaeceegggea 2061
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Best Local Similarity 86.45
Matches 19; Conservative
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                                                                                                                                                                                                                                                                       animal's fodder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
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neuroprotector; immunosuppressor; predisposition; high blood pressure; cardiovascular disease; myocardial infarction; anxiety; depression; neuropsychiatric disease; attention deficit disorder; hyperactivity; eating disorder; anorexia nervosa; bullimia; migraine; allergy; drug; post-traumatic stress disorder; autonomous nervous system disease; metabolic illness; gene therapy; pharmaceutical intervention therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid sequence represented in AAZ00773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid sequence represented in AAZ00773"
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nucleic acid sequence represented in AAZ00773"
replace(934,9)
                                           AAW75777) having an arginine residue at position 16. A novel method for identifying individuals susceptible to adverse responses to regular administration of beta agonists comprises: (a) identifying in a genomic nucleic acid sample from the individual first and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                     comprises determining nucleotide sequences of these portions (e.g. by automated sequence analysis). The invention identifies a known polymorphism in the beta 2-adrenergic receptor gene as being linked
                                                                                                                             second alleles of the beta 2-adrenergic receptor gene, and (b) classifying an individual as susceptible if first and second alleles both encode Arg at residue 16 of the beta 2-adrenergic receptor protein. Beta 2-adrenergic receptor gene alleles may be identified by any known method e.g. denaturing gel electrophoresis or PCR amplification (see also ANV55615-17). Identification preferably comprises amplifying a portion of each allele which includes the sequence encoding residue 16, and optionally also
                   This cDNA sequence codes for human beta-2-adrenergic receptor (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "This nucleotide differs from the wild type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta 2-adrenergic receptor; human; hypotensive; cardiant; stroke;
                                                                                                                                                                                                                                                                                                                                                                                        to adverse responses to regular beta-agonist administration; position 16 of the encoded protein can be either Arg or Gly, and individuals homozygous for Arg16 are more susceptible.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.2; DB 19; Length 3451;
Pred. No. 3.2e+02;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3451 BP; 790 A; 873 C; 895 G; 893 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human beta 2-adrenergic receptor DNA variant 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1410 CTGCCAGTTCCAGCCCGTGCTC 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 cagecagttecacecegtgeae 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(159,t)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replace(565,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.78;
86.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-OCT-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAZ00774;
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Claim 2; Fig 2a; 27pp; German.

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/note= "This nuclectide differs from the wild type
nucleic acid sequence represented in AAZ00773"
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nucleic acid sequence represented in AA200773"
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/note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AAZ00773"
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/note= "This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Ile residue to Thr residue"
                          nucleic acid sequence represented in AA200773"
                                                                /note= "This nucleotide differs from the wild type nucleic acid sequence represented in AA200773"
                                                                                                                    /_cds_ "yis nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding wild type amino acid sequence from an Cys residue to Arg residue"
                                                                                                                                                                                                                                                                             /note= "This nucleotide differs from the wild type
nucleic acid sequence represented in AA200773
and results in a change in the corresponding
                                                                                                                                                                                                                                                                                                                                                                                This nucleotide differs from the wild type nucleic acid sequence represented in AAZ00773 and results in a change in the corresponding
/*tag= e
/note= "This nucleotide differs from the wild type
                                                                                                                                                                                                                                                                                                                                                                                                                        wild type amino acid sequence from an Glu
residue to Gln residue"
                                                                                                                                                                                                                                                                                                                        wild type amino acid sequence from an Gly residue to Arg residue"
                                                                                                                                                                                                                                                                                                                                                                                /note= "This nucleotide differs from the wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human beta2-adrenergic receptor gene variants, useful for determining an individuals haplotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Timmermann B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replace(2826,g)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replace(2078,c)
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                                                                                                                                                                                                 replace(1568,t)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     replace(1839,g)
                                         replace(1221,c)
                                                                                            replace(1541,t)
                                                                                                                                                                                                                                                       replace(1633,a)
                                                                                                                                                                                                                                                                                                                                                       replace(1666,c)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998;
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                                                                                                                                                                                                                                                    mutation
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This invention describes novel variant human beta 2-adrenergic receptor gene sequences which have hypotensive, cardiant, neuroprotective and immunosuppressive activity. The products of the invention are used in a method to determine a predisposition for high blood pressure as well as for abnormal blood pressure and other cardiovascular diseases, including myocardial infarction and stroke. Other conditions that can be determined include neuropsychiatric disease, such as depression, anxiety, attention deficit disorder with hyperactivity, eating disorder. Diseases of the autonomous nervous system, e.g. Bradbury-Egglesston, SNy Drager and Riley-Day syndromes having selective noradrenergic-receptor disposition, or migraine, allergic conditions, e.g. asthma and atopic disorders, and metabolic illnesses, e.g. morbid obesity including predicting a change in weight, using body mass index, can also be determined. The beta 2-adrenergic receptor sequence variants can be used to develop therapeutics and/or lifestyle drugs. Individual specific beta 2-radrenergic receptor approach including gene therapy and pharmaceutical intervention therapy. This sequence represents a variant of the wild type human beta 2-adrenergic receptor gene which is represented in AA200773.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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AZ393372 Rattus no
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Patent: WO 0203785-A 7 10-JAN-2002;
Aventis CropScience GmbH (DE)
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                                                                                                                                                                                                                                                                                          linear PAT 06-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC103298 177696 bp DNA linear HTG 21-DEC-2 Rattus norvegicus clone CH230-75J23, *** SEQUENCING IN PROGRESS ***, 66 unordered pieces.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses Patent: WO 0202785-A 1 10-JAN-2002;
Aventis Cropscience GmbH (DE)
                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 24; DB 6; Length 3785; 100.0%; Pred. No. 3.1;
100.0%; Score 24; DB 6; Length 24; 100.0%; Pred. No. 5.1; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                             DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  961 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                        AX349063 3785 bp
Sequence 1 from Patent WO0202785.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            location/Qualifiers
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                                                                                                         1 tcagccagttccaccccgtgcacg 24
                                                                                                                                                         1 TCAGCCAGTTCCACCCGGTGCACG 24
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                                                                                                                                                                                                                                                                                                                                                              AX349063.1 GI:18615098
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HTG; HTGS_PHASE1.
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Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o 086
                                                   24; Conservative
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     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    bread wheat.
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Helins, B., Homsi, F., Hougson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulk, S., Hume, J., Jackson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Juckson, L. B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Juckson, C., Karlsson, E., Kelly, S., Khan, J., Karlson, B., Lewis, L. Lewis, L. Li, J., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulsegd, H., Lozado, R.J., Lux, Lucier, A., Lucier, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., Martingle, A., Martinez, E., Marsey, E., Mawhiney, E., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuon, G., Oraqunye, N., Nickerson, E., Nwokenkwo, S., Peery, J., Peterz, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Shooshtari, N., Sisson, I., Sodergren, E., Soneike, T., Sparks, A., Stanley, H., Tamerisa, K., Tang, H., Tang, H., Taylor, C., Taylor, T., Tallrod, B., Tamerisa, K., Tang, H., Taylor, C., Taylor, T., Tallrod, B., Tamerisa, K., Wall, K., Wang, S., Walliams, G., Warren, R., Washington, C., Worley, R., Wu, Y., Zorrilla, S., Nelson, D., Pricer, S., Williams, G., Walliams, R., Walliams, G., Walliams, G., Walliams, G., Walliams, G., Walliams, G., W
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NOTE: This is a 'working draft' sequence. It currently consists of 66 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 142002 bases at least Q40 Consensus quality: 151283 bases at least Q30 Consensus quality: 159356 bases at least Q20 Consensus duality: 159356 bases at least Q20 Estimated insert size: 14840; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarcose-fp estimation Quality coverage: 2.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baylor Plaza, Houston, TX 77030, USA
On Dec 21, 2001 this sequence version replaced gi:17062960.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length
contig of 7012 bp in length
gap of unknown length
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gap of unknown length
contig of 4974 bp in length
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
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gap of unknown length
contig of 3240 bp in length
gap of unknown length
contig of 1909 bp in length
gap of unknown length
contig of 3217 bp in length
gap of unknown length
gap of unknown length
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unknown length
of 2024 bp in length
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of 3640 bp
                                                                                                                                                                                                                           of 3037 bp
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unknown ler
of 4181 b
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of 3905 b
unknown 1
                                      unknown lof 4587 kunknown lof 4269 k
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of 4861 h
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of 3092 b
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of 5480
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of 2600
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of 2720 l
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of 1849
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of 2192
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                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 2343
gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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               contig
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60046
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65007
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Giardia intestinalis clone CI0266 ștrain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-APR-2000) to the EMBL/GenBank/DDBJ databases. Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crocker M.K., Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                       Score 19.2; DB 2; Length 177696; Pred. No. 2.7e+02; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Giardia intestinalis
Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                            length
op in length
                       ength
p in length
            in length
                                                   in length
                                                                                                               ín length
                                                                                            in length
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bp in length
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length
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                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                unknown length
of 1378 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This record contains 1 individual * sequencing reads that have not been assembled into
                                          Length
                                                                                   ength
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                                                                                                                                                                   length
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05-APR-2000 (Rel. 63, Last updated, Version 1)
                                                  of 1932 l
unknown
                                                                                                    unknown
of 2012
                                                                                                                of 2012 |
unknown
of 1903 |
                                                                                                                                             unknown
of 1127 b
unknown
of 1525 b
                                                                                                                                                                                     unknown l
of 1417 h
unknown l
of 1013 h
                                                                                                                                                                                                                   of 1013 l
unknown l
of 1490 h
                      unknown
of 1173
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of 1309
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of 1378
                                                                        1276
                                           unknown
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AC028268/c
ID AC028268 standard; DNA; HTG; 959 BP.
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gap of
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163643:
163743:
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158045:
159462:
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87.5%;
                               146161:
                                                   148193:
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                                                                                                                                                                                                                                         162165:
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Best Local Similarity 87.5
Matches 21; Conservative
142743
142843
144889
144686
146262
148194
148294
149570
1149570
1151079
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158046
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155094
155194
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160576
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162266
163644
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AC028268.1
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HTG; HTGS_PHASE0
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                         be preserved.
                                                                                                                                                      Sequence 960
                                                                                                                                                                                                                                                                                                                                                                   AC072500.1
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                                                                                                                                                                                       Query Match
                                                                                    source
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                                                                                                                                                                                                               Matches
                                                             Key
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                                                                                                                                                                                                                                                                                               RESULT
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  Giardia intestinalis clone AJ2336 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-SEP-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MCArthur A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                             78.3%; Score 18.8; DB 33; Length 959; 90.9%; Pred. No. 6.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 1 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
                                                                                                                                                                                                                          Sequence 959 BP; 226 A; 251 C; 259 G; 216 T; 7 other;
                                                                        * will be sequenced to completion. In the event that
                                                           · However, it should not be assumed that this clone
                                                                                    * the record is updated, the accession number will
                                                                                                                                                                           /organism="Giardia intestinalis" /strain="WB-C6"
                                                                                                          959: contig of 959 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-2000 (Rel. 65, Created)
29-SEP-2000 (Rel. 65, Last updated, Version 1)
                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; HTG; 960 BP.
                                                                                                                                                                  /db_xref="taxon:5741"
                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                      /clone="CI0266"
                                                                                                                                                                                                                                                                                                                                    265 AGCCAGGTCGACCCCGTGCACG 244
                                                                                                                                                                                                                                                                                                              3 agccagttccaccccgtgcacg 24
                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Giardia intestinalis
                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AC080286.1
                                                                                                                                                                                                                                                                                                                                                                                            AC080286
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                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                    Key
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Giardia intestinalis clone NJ4295 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18.8; DB 33; Length 960;
Pred. No. 6.7e+02;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (07-JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence ampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                     BP; 219 A; 256 C; 248 G; 237 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           will be sequenced to completion. In the event that
* will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                However, it should not be assumed that this clone
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                              * the record is updated, the accession number will
                                                                                                                                                                                                                                                                              /organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          972: contig of 972 bp in length.
                                                                                           960: contig of 960 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-2000 (Rel. 64, Created)
13-JUN-2000 (Rel. 64, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 * NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA; HTG; 972 BP.
                                                                                                                                                                                                                                                             /db_xref-"taxon:5741"
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                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            /clone="AJ2336"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.3%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                               . 960
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nes 20; Conserva
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Giardia intestinalis clone EJ6686 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-JUN-2000) to the EMBL/GenBank/DDBJ databases.
Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eakin N.Q., Morrison H.G., McArthur A.G., Nixon J., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                         0
                                                                                                                                                      Score 18.8; DB 33; Length 972;
Pred. No. 6.7e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                       Sequence 972 BP; 221 A; 250 C; 268 G; 231 T; 2 other;
                            /db_xref="taxon:5741"
/organism="Giardia intestinalis"
/strain="WB-C6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Giardia intestinalis"
/strain="WB-C6"
/clone="EJ6686"
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13-JUN-2000 (Rel. 64, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This record contains 1 individual
                                                                                                                                                                                                                                                                                                                          standard; DNA; HTG; 990 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:5741"
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                                                                           /clone="NJ4295"
                                                                                                                                                                                                                               460 AGCCAGATCGACCCGTGCACG 481
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                                                                                                                                                                                                                 3 agccagttccaccccgtgcacg 24
                                                                                                                                                  Query Match 78.3%;
Best Local Similarity 90.9%;
Matches 20; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved.
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ID AC070455
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323450 bp DNA linear BCT 16-AUG-2001
Sincorhizoblum meliloti 1021 complete chromosome; segment 9/12.
AL591790 AL591688
AL591790.1 GI:15075737
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Boistard,P., Becker,A., Boutry,M., Cadieu,E., Dreano,S., Gloux,S.,
Godrie,T., Goffeau,A., Kahn,D., Kiss,E., Lelaure,V., Masuy,D.,
Pohl,T., Portetelle,D., Puehler,A., Purnelle,B., Ramsperger,U.,
Renard,C., Thebault,P., Vandenbol,M., Weidner,S. and Galibert,F.
From the Cover: Analysis of the chromosome sequence of the legume
symbiont Sinorhizobium meilloti strain 1021
Proceedings of the National Academy of Sciences of the United
11481430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratolize de Biologie Moleculaire des Relations
Plantes-Microorganismes, UMR215-CNRS-INRA, BP27, F-31326 Castanet,
France, Laboratolize de Genetique et Developement UMR6061-CNRS,
Fraulte de Medecine, 2 avenue du Pr. Leon Bernard, F-35043 Rennes,
Universitate Bielefeld, Biologie IV (Genetik) Universitatetstr 25,
Universite Catholique de Louvain, Place Croix du Sud 2, Bte 20,
B-1348 Louvain-la-Neuve, Belgium, Unite de Microbiologie, Faculte
des Sciences Agronomiques de Gembloux, Avenue Marechal Juin 6,
B-5030 Gembloux, Belgium. E-mail:Genome, Gouzyétoulouse.inra.fr
http://sequence.toulouse.inra.fr/meliloti.html.
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/note="Product confidence : hypothetical
Gene name confidence : hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                  Gaps
                                                                                                                                             ;
0
                                                                                                Length 990;
                                                                                                                                                Indels
                    Sequence 990 BP; 228 A; 273 C; 282 G; 206 T; 1 other;
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                                                                                             Score 18.8; DB 33;
Pred. No. 6.7e+02;
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                                                                                                                                             0; Mismatches
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predicted by Homology
predicted by FrameD"
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1. .323450
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1 (bases 1 to 323450)
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/gene="SMc01575"
155. .1519
/gene="SMc01575"
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                                                                                             78.3%;
90.9%;
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                                                                                      Query Match 78.3'
Best Local Similarity 90.9'
Matches 20; Conservative
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AUTHORS
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JOURNAL
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KEYWORDS
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gene

CDS

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ALHLAETGIRTAVIEARMIGFGGSGRNVGLVNAGWWQPDDLIATLGAAAGNRLLDEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNLKTPRGTVTARHVILATNAYGSLYTGVPWKEYRQELTILPYFQFATNPLPDNVAAR
ILPERQCAWDTGLVWTSFRMDRQNRLIFGSIGRLDA1AAGTHRAFAARSVRKLFPYIG
BAFREHWWDGRIGMTYNNLPAAHVLAPNVVSIGGYNGRGIAPGTVFGRALARHVTGDT
SAIPLAETPVTPDPWTLKSAFYHAGAQAKHFIDKRF"
complement(3024, 3740)
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YSWSSVSGRYANLEVISHYPPASLCPHIREKGENFTVIDIAGAKNDA VALALGLSD
HVLIPVOGCAMDARGAVQILELIRHIGEKARYRINSSYVLRYNSIVTTRALOTIKAL
LASRGVSVLDFPIVERVAYREIFEGGGTLQMMDPNRVSNLDKARENAYALAAEVQNLL
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LAQPWPPAMTVTGK SRAEIAALQVFLDREGFSPGVIDGKMGSNVTKA I EAWQQATGET
                                                                                                                                                    LDPNNTEDILERLRFNGGLPITTTITAADAAGPFVASIPEDYAHKAQLPHLSFTSVT
BEMGERKHNDERVLRELNPGVDFSIGGTTIKVVNPGPNKKGKVARIVARKAKOYLAY
DEAGKLIAAYPSTIGSSDTPGSGTVHVPRIAFDFDGYTYNPK INFOGANDRILOLOG
GPNGPVGTVWIALSKPTYGIHGTPEPSKIGKTQSHGCVRLTNWDATELGKMVSTGVTV
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Gene name confidence: hypothetical
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predicted by Homology
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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/note="Product confidence : putative
Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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/gene="SMc01576"
1707. ?occ
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KEVREIPHTLREAGEALSGSKMLRAAFGEEVVDHYVHAAEWEQQEYDRRYTDWEVARG
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AWKETHSCNYLLATDMEMETVPGYKATSWEKGYGDYTMKPDLSTLRRIPWLEGTALVL
CDMLDHDTHAEVPHSPRAILKKQVARLEAMGFKAYMASELEFFLFDGSYDDARLSGYR
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APSTEKSVAWSNYKLONPLDETTLCBMANKREAATVRNOVADAISKGARALIDPKL
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IYNTHHGMTNAVVMPPVLRFNRSATEEKIGRAAAYLGTAGGFDGFYDYVLRLREELGV
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PMAITQQALDILEAGGLGRAIFADVDPNPNDRNLEAGVKAFRDGGHDGVVAFGGGSGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(6674. .8038)
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complement(6674. .8038)
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complement(5091. .6476)
/gene="SMc01588"
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/note="Product confidence : putative
Gene name confidence : hypothetical
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Gene name confidence : hypothetical
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Pred. No. 3.8e+02;
0; Mismatches 2;
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predicted by Homology
predicted by FrameD"
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predicted by Homology
predicted by FrameD"
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predicted by Homology
predicted by FrameD"
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ACLU1702 113288 bp DNA linear HTG 23-NOV-2001 Mus musculus clone RP23-247G20, LOW-PASS SEQUENCE SAMPLING. AC101702
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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771 1437: contig of 667 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                          Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-247G20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L17246
Center clone name: 247_G_20
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                                                                   DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giardia intestinalis clone LJ0406 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis"; Unpublished.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nixon J., Morrison H.G., McArthur A.G., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No. 1e+03;
1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (06-FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-FEB-2001 (Rel. 66, Created)
07-FEB-2001 (Rel. 66, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This record contains 1 individual
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/db_xref="taxon:5741"
                                                                                                                                                                                                                                                       standard; DNA; HTG; 932 BP
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   466 AGCCAGATCGACCCCKTGCACG 445
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1825 19024: gap of 100 bp 11 length 19025 19703: contig of 679 bp in length 1902 19703: contig of 679 bp in length 190804 20518: contig of 715 bp in length 20518: gap of 100 bp 2133 21332: contig of 714 bp in length 2133 21342: gap of 100 bp 2133 2234: gap of 100 bp 2235 2294: gap of 100 bp 2235 2294: gap of 100 bp 2235 22917: contig of 683 bp in length 23018 23079: gap of 100 bp 23018 23778: contig of 691 bp in length 23709 23808: gap of 100 bp 23608: gap of 100 bp 23608: gap of 24695: contig of 687 bp in length 23695: contig of 687 bp in length 23695: contig of 687 bp in length
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of 100 bp
contig of 679 bp in length
of 100 bp
contig of 695 bp in length
                                                                                                                                                                                                                                                                                                                                           of 100 bp contig of 702 bp in length
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                                                                                                                                          of 100 bp contig of 692 bp in length
                                                                                                                                                                                                              of 100 bp contig of 704 bp in length
                                                                                                                                                                                                                                                                              of 100 bp contig of 688 bp in length
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                                   38.

4572.

4672.

4672.

5367 5466:

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6159 6259. con.

6259 6962: con.

6963 7062: gap of

7850: gap of

8521: con.

7850: gap of

8521: con.
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28618 29334: conti
29335 29434: gap of
29435 30116: conti
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       3793 3892:
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26203
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ละบงษวชง 233684 bp DNA linear HTG 16-NOV-2001
Mus musculus clone RP23-189G16, WORKING DRAFT SEQUENCE, 25
unordered pieces.
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Pred. No. 6.3e+02;
); Mismatches 1; Indels 0;
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50096: contig of 720 bp in length
196: gap of 100 bp
19903: contig of 707 bp in length
103: gap of 100 bp
51660: contig of 657 bp in length
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54843: contig of 713 bp in length
54943: gap of 100 bp
                                in length
                                                                                               in length
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                                                                                                                                                                                                                                                                                      in length
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                                                                                                                                                                                                                                                                                                                                                                        1153: gap of 100 bp
3887; contig of 704 bp ii
91957: gap of 100 bp
39666: contig of 709 bp ii
766: gap of 100 bp
                                                                                                                                                                                                                                                  ap of 100 bp
:: contig of 718 bp 1:
ap of 100 bp
:: contig of 691 bp ii
33358: gap of 100 bp
34077: contig of 719 bp
34177: gap of 100 bp
34887: contig of 710 bp
                                                                                                                            34987: gap of 100 bp
35656: contig of 669 bp
35756: gap of 100 bp
36444: contig of 688 bp
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                                                                                                                         34987; gap of
35656; cont
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37262: cont
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38053: cont
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50096: cont
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53255: cont
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54844 54943: gap of
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Matches 19; Conservative
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REFERENCE

KEYWORDS

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76303; gap of 100 bp 197144; contig of 20841 bp in length 27144; gap of 100 bp 221039; contig of 23395 bp in length
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150868: contig of 21506 bp in length
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                                  5093 6602: Coulty 100 bp
6603 6702: app of 100 bp
6703 10246: contig of 3544 bp in length
6703 10346: app of 100 bp
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12130 12229: gap of 100 bp
1223 bp in length
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27548: contig of 4085 bp in length
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of 100 bp
contig of 1510 bp in length
                                                                                                                       10247 10346: gap of 100 bp
10347 12129: contig of 1783 bp in length
                                                                                                                                                                                                                                                        14554: gap of 100 pp
16558: contig of 2004 bp in length
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/note="assembly_fragment"
1455s. .16588
/note="assembly_fragment"
16659. .19755
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23464. .27548
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hote="assembly_fragment"
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/note="assembly_fragment"
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'note="assembly_fragment"
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/db_xref="taxon:10090"
/clone="RP23-189G16"
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559. .2100
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Signature, Inton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastlen, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamata, A., Karatas, A., Kalls, C., Lakoque, K., Landers, R., Ladders, T., Lendersky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacBan, P., McKernan, K., MoPheeters, R., Madlatim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Ollver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V., Raymond, C., Rette, R., Rieback, M., Riley, R., Rise, C., Schupback, R., Schauer, S., Severy, P., Spencer, B., Stange-Thoman, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Pierre, S., Shiphele, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (16-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 233684)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 240000; agarose-fp
Insert size: 231284; sum-of-contids
Quality coverage: 11.5 in Q20 bases; agarose-fp
Quality coverage: 11.9 in Q20 bases; sum-of-contigs
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-189G16
      HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                              AUTHORS
TITLE
                                                                                                                                                                                                                                                               JOURNAL
REFERENCE
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COMMENT

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Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens genomic sequence surrounding NotI site, clone HSJ-DG20RS.
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                                                                                                                                                                               * identifying clones that may be gene-rich and allows voratap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that
                                                                                                * sequencing reads that have not been assembled into acontigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 667 BP; 159 A; 143 C; 183 G; 176 T; 6 other;
                                                                                                                                                                                                                                                                 * the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                         667: contig of 667 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:5741"
/organism="Giardia intestinalis"
/strain="WB-C6"
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                                                                               * NOTE: This record contains 1 individual
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/db_xref="taxon:9606"
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239 c 217 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="AJ2486"
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87.0%;
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                                                                                                                                                                                                                                                                                        be preserved.
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                     Giardia intestinalis clone AJ2486 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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02-AUG-2000 (Rel. 64, Last updated, Version 1)
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/note="assembly_fragment"
27649. .31362
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standard; DNA; HTG; 1102 BP
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Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
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Hinkle G., Holder M.E., Sogin M.L.;
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Pred. No. 1.2e+03;
0; Mismatches 3; Indels 0;
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/strain="WB-C6"
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26-APR-2000 (Rel. 63, Last updated, Version 1)
  0; Mismatches
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Giardia intestinalis clone AJ2681 strain WB-C6, LOW-PASS SEQUENCE SAMPLING.
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Josephine Bay Paul Center for Comparative Molecular Biology and Evolution,
Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA
                                                                                                                                                                                                                                                                                                                                                                                Morrison H.G., McArthur A.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C., Hinkle G., Holder M.E., Sogin M.L.; "Giardia: a model for ancient eukaryotic genome analysis";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCARThur A.G., Morrison H.G., Nixon J., Eakin N.Q., Kim U., Crocker M.C.,
Hinkle G., Holder M.E., Sogin M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                      Eukaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying olnes that may be generate and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1102 BP; 294 A; 283 C; 258 G; 265 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18.2; DB 33;
Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1102: contig of 1102 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Giardia intestinalis"
02-AUG-2000 (Rel. 64, Created)
02-AUG-2000 (Rel. 64, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:5741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              546 TCAGCCAGTGCCCCCGCGTGCAC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="WB-C6"
/clone="AJ2681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 tcagccagttccaccccgtgcac 23
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87.0%;
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Best Local Similarity 87.0
Matches 20; Conservative
                                                                                                                                                                                                                           Giardia intestinalis
                                                                                                                                                              HTG; HTGS_PHASE0
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:23:47; Search time 165.21 Seconds (without alignments) 17.842 Million cell updates/sec Run on:

US-09-899-718A-6 12 1 caggagcctcga 12 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

383533 seqs, 122816752 residues Searched:

767066 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* Issued_Patents_NA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

			đ			SUMMAKIES	
Result No.	ult No.	Score	Query Match	Query Match Length	DB	ΩI	Description
; 0	1	12	100.0	475	4	US-09-247-155-147	Sequence 147, App
O	71	12	100.0	1341	4	US-09-199-637A-266	266,
	٣	12	100.0	1722	4	US-09-221-275-3	3, 19
O	4	12	100.0	2001	4		7
	Ŋ	12	100.0	2671	4	US-09-221-275-2	7
	9	12	100.0	2678	4	US-09-221-275-1	1, 1
υ	7	12	100.0	3116	C	US-08-449-645A-14	14,
O	œ	12	100.0	3116	~	US-08-702-367A-14	14,
บ	σ	12	100.0	3116	Ŋ	PCT-US95-04681-14	14,
U	10	12	100.0	3348	Н	US-08-222-616-34	34,
υ	11	12	100.0	3348	Ŋ	PCT-US95-04228-34	34,
O	12	12	100.0	3995	4	US-09-428-711A-13	13,
	13	12	100.0	4680	٦	US-08-254-358-1	Sequence 1, Appli
	14	12	100.0	4680	Н	US-08-475-391-1	ı,
	15	12	100.0	4680	7	US-08-709-609-1	ı,
	16	12	100.0	4680	Ŋ	PCT-US95-07178-1	'n
υ	11	12	100.0	5802	4	US-09-341-587-4	4
D	18	12	100.0	28720	4	US-09-341-587-7	7,
O	19	12	100.0	42235	4	US-09-199-637A-1	1,
ပ	20	11	91.7	30	ო	-80-	10,
υ	21	11	91.7	97	-	US-08-370-975B-9	σì
ပ	22	11	91.7	334	~+	US-08-358-171-22	22,
υ	23	11	91.7	334	3	947	22,
O	24	11	91.7	340	Н	US-08-594-031-83	83,
	25	11	91.7	412	Н	US-08-047-041A-1	Sequence 1, Appli
	26	11	91.7	412	7	US-08-795-006A-21	21,
	27	11	91.7	412	4	US-09-184-073-21	Sequence 21, Appl

	, Appl	, Appl	, Appl	, Appl	Appli	Appli	Appli	Appli	, Appl	Appli	, Appl	Appli	Appli	, Appl	, Appl	Appli	Appli	Appli	
,	15	14	13	14	6	ó	6	6	13	æ	19,	'n	H	13	13,	9	ı,	ľ,	
	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Sequence	Sednence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sednence	Sequence	Sednence	Seguence	
	US-08-892-880-12	US-08-047-041A-14	US-08-370-975B-13	US-07-661-610C-14	US-09-609-324A-9	US-08-920-440B-9	US-09-173-492-9	US-09-173-133-9	US-09-269-617-13	US-08-278-630A-8	US-09-372-422A-19	US-08-356-180-1	US-08-892-880-1	US-08-765-662-13	PCT-US95-08745-13	US-08-941-445A-6	US-08-808-982-1	US-09-306-902A-1	
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	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	91.7	
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# ALIGNMENTS

E E	RESULT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
. č	Sequence 147, Application US/09247155A
	; Patent No. 6312922
	GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, Jean-Baptiste
	APPLICANT: Duclert, Aymeric
٠.	APPLICANT: Bougueleret, Lydie
•-	TITLE OF INVENTION: Complementary DNAs
٠.	FERENCE: GENSET.021A
• •	CURRENT APPLICATION NUMBER: US/09/247,155A
٠.	FILING DATE: 1999-02
	EARLIER APPLICATION NUMBER: 60/074,121
	FILING DATE: 1998-04
٠.	
٠.	FILING DATE: 1998-08
••	EARLIER APPLICATION NUMBER: 60/099,273
	-10
••	
••	SOFTWARE: Patent.pm
••	SEQ ID NO 147
••	LENGTH: 475
••	TYPE: DNA
••	ORGANISM: Homo sapiens
•	
٠.	NAME/KEY: CDS
••	LOCATION: 146457
••	FEATURE:
٠.	NAME/KEY: sig_peptide .
••	146292
••	INFORMATION:
••	INFORMATION: SCO
٠.	FORMATION:
٠.	FEATURE:
٠.	NAME/KEY: polyA_signal
•-	
••	FEATURE:
•-	NAME/KEY: polyA_site
٠- ;	; LOCATION: 465475
ö	S-09-247-155-147

Gaps 0; Query Match 100.0%; Score 12; DB 4; Length 475; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 12; Conservative 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                                                                                LENGTH
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                                                                                                                                                                                                                 APPLICANT: Manual Mathematical Applicant: Manual Mapulcant: Tan, Manual Mapulcant: Cao, Hui Mapulcant: December of Eliana Applicant: Tsongalis, John TILLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID TILLE OF INVENTION: SEQUENCES AND USES THEREOF FILE REPERENCE: 00786/361002 CURRENT FILING DATE: 1998-11-25 PRIOR APPLICATION NUMBER: 60/066,517 PRIOR APPLICATION NUMBER: 60/066,517 NUMBER OF SEQ ID NOS: 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bodie, Elizabeth A. APPLICANT: Graycar, Thomas P. APPLICANT: Winetzky, Deborah S. TITLE OF INVENTION: Pleurotus Phenol Oxidizing Enzymes FILE REFERENCE: GC557
CURRENT APPLICANTION NUMBER: US/09/221,275
CURRENT FILIG DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 12; DB 4; I
100.0%; Pred. No. 1.4e+02;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 12; DB 4; 100.0%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                RESULT 2
US-09-199-637A-266/c
; Sequence 266, Application US/09199637A
; Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09221275 Patent No. 6329332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Pseudomonas aeruginosa US-09-199-637A-266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Borneman, William S.
APPLICANT: Bodie, Elizabeth A.
                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick
APPLICANT: Goodman, Howard M.
APPLICANT: Rahme, Laurence G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 12; Conservative
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Best Local Similarity 100.
Matches 12; Conservative
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SEQ ID NO 3
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LENGTH: 1341
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US-09-221-275-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 12; DB 4; Length 20 100.0%; Pred. No. 1.4e+02; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Borneman, William S.
APPLICANT: Borneman, William S.
APPLICANT: Bodie, Elizabeth A.
APPLICANT: Graycar. Thomas P.
APPLICANT: Winetzky, Deborah S.
TITLE OF INVERTION: Pleurotus Phenol Oxidizing Enzymes FILE REFERENCE: GC557
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Borneman, William S.
APPLICANT: Bodie, Elizabeth A.
APPLICANT: Graycar, Thomas P.
APPLICANT: Winetzky, Deborah S.
TITLE OF INVENTION: Pleurotus Phenol Oxidizing Enzymes FILE REFERENCE: GC557
                                                                                          GENERAL INFORMATION:
APPLICANT: MOllenhauer, Jan
TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REPERENCE: 4121-108
CURRENT APPLICATION NUMBER: US/09/341,587
CURRENT FILING DATE: 1999-08 31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-221-275-2; Sequence 2, Application US/09221275; Patent No. 632933; GENERAL INFORMATION:
RESULT 4
US-09-341-587-2/c
5 Sequence 2, Application US/09341587
Patent No. 6346606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  // Sequence 1, Application US/09221275
// Patent No. 6329332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pleurotus ostreatus
US-09-221-275-2
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SEQ ID NO 2
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; ORGANISM: Homo sapiens
US-09-341-587-2
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Best Local Similarity
Matches 12; Conserv
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LENGTH: 2671
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                             ZIP: 91320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION:
US-08-702-367A-14
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                                                                                                                                                                                                          Length 2678;
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                                                                                                                                                                                                                                                                                                                                                                             US-08-449-645A-14/C

| Sequence 14, Application US/08449645A
| Patent No. 5981245
| GENERAL INFORMATION:
| TILLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine:
| TITLE OF INVENTION: Aluases
| NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Amgen Patent Operations/RBW |
| STREET: 1840 Dehavilland Drive |
| COUNTRY: USA
                                                                                                                                                                                                     100.0%; Score 12; DB 4; Length 26
100.0%; Pred. No. 1.4e+02;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
CURRENT APPLICATION NUMBER: US/09/221,275
CURRENT FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 8
SEQ TWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Application US/08702367A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRENDEDNESS: single
                                                                                                          ; TYPE: DNA
; ORGANISM: Pleurotus ostreatus
US-09-221-275-1
                                                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
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34..2994
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Matches 12; Conserv
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US-08-449-645A-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Ouery Match
Best Local Similarity 100.0%; Score 12; DB 1; Length 3348;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US95/04228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                821P3PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEE: Genentech, Inc.
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                             Sequence 34, Application PC/TUS9504228 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 13, Application US/09428711A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/222615
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 821P
TELECOMMUNICATION INFORMATION:
TELEPRONE: 415/252-1994
TELEPRAX: 415/952-9881
TELERX: 910/371-7168
INPORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      Bennett, Brian D.
Goeddel, David
                                                                                                                                                                                                                                                                                                                                       Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGIH: 3348 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         698 CAGGAGCCTCGA 687
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-428-711A-13/C
                                                                                                                                                                                                                                                          RESULT 11
PCT-US95-04228-34/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
PCT-US95-04228-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94080
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                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
US-08-222-616-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Wood, William
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAPLICATION NUMBER: US/08/222,616
FILING DATE: 4-APR-1994
CLASSIPICATION: 530
PRIOR APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
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REFERENCE/DOCKET NUMBER: 821P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1994
TELEPAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34, Application US/08222616 Patent No. 5635177
  REFERENCE/DOCKET NUMBER: A-287 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 3348 bases
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                                                                                                                                                        MOLECULE TYPE: CDNA
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TOPOLOGY: linear
                                                                                                                                    linear
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                                                                                                                                                                                                  NAME/KEY: CDS
                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94080
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                                                                                                                                  TOPOLOGY:
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Gaps
0; Gaps
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APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVERTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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PROGRAMMER: 08/254,358
APPLICATION DATA:
APPLICATION NUMBER: 08/254,358
ATTING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 578621land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (312) 474-6300
TELESAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGH: 4680 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLEGULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-475-391-1
LENGTH: 4680 base pairs
                                                                                                                                                                 Query Match
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 12; Conservative
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US-08-254-358-1
US-08-254-358-1
; Sequence 1, Application US/08254358
; Patent No. 5558785
; GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Methods
; TITLE OF INVENTION: Methods
; NUMBER OF SEQUENCES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: Chicago
CITY: Chicago
STATE: 1111nois
COUNTRY: USA
ZIP: 60666
CCOMPUTER FF
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                                  APPLICANT: Muramatsu, Masaaki
APPLICANT: Shirasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: Tokumitsu, Hiroshi
APPLICANT: No. 6358720uchi, Teruhisa
TITLE OF INVENTION: SENTINE/THREONINE PROTEIN KINASE
FILE REFERENCE: 06501-045001
CURRENT APPLICATION NUMBER: US/09/428,711A
CURRENT FILING DATE: 1999-10-28
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PCT/TP98/01246
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION DATA:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 12; DB 4; I
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIPICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: NO. 558785and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31975
TELEPHONE: (312) 474-6300
TELEPAX: (312) 474-6300
TELEPAX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(3995)
; OTHER INFORMATION: n = A,T,C or G
US-09-428-711A-13
                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: CDS
LOCATION: (388)...(3540)
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Mus musculus
                 GENERAL INFORMATION:
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LENGTH: 3995
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US-08-475-391-1
Sequence 1, Application US/08475391
Fatent No. 5786211
GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 S. Wacker Drive
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100.0%; Score 12; DB 1; Length 4680; 100.0%; Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/08/475,391
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                                        0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Johnson, Philip R.
TITLE OF INVENTION: Adeno-Associated Virus Materials and
TITLE OF INVENTION: Methods
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PARTENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: NO. 5859775and, Greta E.
REGISCRATION NUMBER: 35,302
REFERENCE/COCKET NUMBER: 31975
TELECOMMUNICATION INFORMATION:
TELECHONE: (312) 474-6300
TELERA: (480 Date: 1: SEQUENCE CHARACTERISTICS: LENGTH: 4600 Date: 2 LENGTH: 1 TYPE: nucleic acid
STRANDENESS: single
             ; Sequence 1, Application US/08709609
; Patent No. 5858775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-709-609-1
                                                                                                                                                                                                                                                                                    CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
US-08-709-609-1
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Query Match 100.0%; Score 12; DB 2; Length 4680; Best Local Similarity 100.0%; Pred. No. 1.4e+02; Matches 12; Conservative 0; Mismatches 0; Indels (

1 caggageetega 12 ŏ

Db 2993 CAGGAGCCTCGA 3004

Search completed: July 31, 2002, 12:23:49 Job time: 11852 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

July 31, 2002, 12:12:05; Search time 5855.71 Seconds (Without alignments) 27.659 Million cell updates/sec

US-09-899-718A-6 12 1 caggagcctcga 12 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

gb_gss:* em_gss_hum:* em_gss_inv:* 1: em_estba:*
2: em_esthum:*
4: em_esthum:*
5: em_estru:*
6: em_estco:*
7: em_estro:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:* EST:*  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_pln:* em_gss_vrt:*

SUMMARIES

			dР				
ž	Result No.	Score	Query Match	Query Match Length DB		ΙD	Description
	, , , , , , , , , , , , , , , , , , ,	12	100.0	109	10	BF371310	BE371310 RC6-FN011
	7	12	100.0		12	AZ747991	AZ747991 RPCI-24-1
J	c 3	12	100.0		12	BH354246	
	4	12	100.0		12	AZ748898	AZ748898 RPCI-24-1
	വ	12	100.0		0	AA584951	AA584951 nn41b12.s
	ø	12	100.0		10	BI518243	BI518243 603042090
	7	12	100.0		10	BF812758	BF812758 CM2-CI018
J	<b>ω</b>	12	100.0		10	BF926690	BF926690 PM1-NT023
	σ	12	100.0		10	BE827454	BE827454 CM2-ET001
	10	12	100.0		10	BI002833	BI002833 MR3-HN016
	11	12	100.0		12	AZ271167	AZ271167 RPCI-23-4
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	14	12	100.0		σ	AA074114	AA074114 zf79f05.r
	12	12	100.0		σ	AA657774	AA657774 nu06f04.s
J	c 16	12	100.0		σ	BB592607	BB592607 BB592607
Ĭ	c 17	12	100.0	211	σ	AA770456	AA770456 ah89f12.s

9 7 2 3 3 3 5 3 7 6 7 7 6 7 7 6 7 7 8 7 7 8 7 8 7 8 7 8	AA356282 EST76054 AV735802 AV735802 BE143676 MRO-HT016 BI008774 VOY3 FKT006 AA348160 EST54567 AA365578 EST76401 BB590276 BB590276 AI564849 tm86a06.x AW325543 17495 MAR R22443 yh23906.s1
	AA365282 AV735802 BE143676 BI008774 AA348160 AA365578 BB59076 AT564849 AW325443
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## ALIGNMENTS

	0	BF371310.1 GI:11333244 EST. human.	Homo sapiens Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 109) Dias Neto, E., Garria Correa, R., Verjovski-Almeida, S., Briones, M.R.,	Nagalm.A., da Sllva.W. Jr., Zago.m.A., Bordin.S., CoSta.F.E., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira.P.S., Bucher,P., Jongeneel.C.V., O'Hare	.M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson a J	Shotgun sequencing of the human transcriptome with ORF expressed	sequence tags Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)	20202663	Contact: Simpson A.J.G.	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,	BIGZII Tel: +55-11-2704922	Fax: +55-11-2707001	Email: asimpson@ludwig.org.br This sequence was derived from the FAPESP/LICR Human Cancer Genome	Project. This entry can be seen in the following URL	(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6st2=RC6-FN0114- 090800-011-E11st3=2000-08-09st4=1)	Seq primer: puc 18 forward	High quality sequence stop: 65.	Location/Qualiflers 1109	/organism="Homo sapiens"
RESULT 1 BF371310/c	LOCUS DEFINITION ACCESSION	VERSION KEYWORDS SOURCE	ORGANISM	REFERENCE AUTHORS			TITLE	JOURNAL	MEDLINE	COMMENT										FEATURES	

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Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., de Jong,P. and Fraser,C.M. Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                         GSS 03-DEC-2001
                                                                                                                                                                                                                                                                                                                       CH230-68019.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-68019, DNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 68 row: 0 column: 19
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                                                  Length 110;
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Tel: 301 838 0200
Fax: 301 838 0208
                                                  100.0%; Score 12; DB 12; 100.0%; Pred. No. 8.7e+03;
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                                                                                               0; Mismatches
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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                                             Query Match
Best Local Similarity 100.0
Matches 12; Conservative
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                                                                GSS 25-JAN-2001
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/note="Wector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2hao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
Russell,D., de Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A2747991 110 bp DNA linear GSS 25-JAN-200:
RPCI-24-125D2.TV RPCI-24 Mus musculus genomic clone RPCI-24-125D2,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
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Unpublished (1999)
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/clone_lib="RPCI-24"
/db_xref="taxon:9606"
/clone_lib="FN0114"
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                                             /dev_stage="Adult"
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ORIGIN

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Best Local Similarity
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SANILAR TO SW:DHCA_MOUSE P48758 CARBONYL REDUCTASE;, MRNA
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AZ748898 125F2.TV RPCI-24 Mus musculus genomic clone RPCI-24-125F2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/GJ
DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: szhaoetigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejongemail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 125 row: F column: 2
Seq primer: T7
                                                                                                                                                                                                                                               Theo,S., Mierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Mussell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-125F2.TJ
Contact: Shaying Zheo
Department of Eukaryotic Genomics
The Institute for Genomic Research
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 133)
                                                                                                                                                               Mus musculus
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
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/clone_lib="RPCI-24"
/sex="Male"
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1. .129
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="IAaxon:9606"
/clone="IMAGE:1086431"
/clone=lib="NoT_CGAP_GGS"
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/lab_host="Solk (kanamycin resistant)"
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/note="Vector: Bluescript SK-; Site_1: CORI; Site_3: XhoI
/note="Vector: Bluescript SK-; Site_1: CORI; Site_2: XhoI
/note="Vector: Bluescript SK-; Site_
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                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the LIM.A.G.E. Consortium/LLNL at:
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbz-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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                                                                                               Tumor Gene Index
Unpublished (1997)
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source

FEATURES

BASE COUNT

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Gaps ; EST 19-JAN-2001

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/note="Organ: Colon_ins; Vector: puc18; Site_1: Smal; Site_2: Smal: A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM1&t2=PM1-NT0235-011200-002-a10&t3=2000-12-01&t4=1)
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PM1-NT0235-011200-002-a10 NT0235 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 153)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/db_xref="taxon:9606"
/clone_llib="NT0235"
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High quality sequence start: 13
High quality sequence stop: 152.
Location/Qualifiers
      /dev_stage="Adult"
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BF926690.1 GI:12324010
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Matches 12; Conservative
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CM2-C10180-221100-540-b07 C10180 Homo sapiens CDNA, mRNA sequence.
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Gordin, S., Costa, F.F., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.Y., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Seq primer: puc 18 forward
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Liocation/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                               /clone="IMAGE:5182415"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
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Location/Qualifiers
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Fax: +55-11-2707001
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-&t2-CM2-ET0016-310
Seq primer: puc 18 forward
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Shotgun sequencing of the human transcriptome with ORF expressed
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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llarity 100.0%; Pred. No. 9.8e+03;
Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"

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/clone_llb="HN0166"

/dev_stage="Adult"

/note="Organ: head_normal; Vector: pucl8; Site_l: Smal;

Site_l: Smal; A mini-library was made by cloning products

Site_l: Smal; A mini-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of tissue mRNR and cDNA amplification were performed under

low stringency conditions.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Diass Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the following URL
Project. This entry oran be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-MR3&t2=MR3-HN0166-
310101-002-e06&t3=2001-01-31&t4=1)
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Liaboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Contact: Erika Asamizu
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                                                                                 Zha', S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV640236 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas reinhardtii cDNA clone HCL012fil_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
                                                                                                                                                                                                                                                                                                                                                                                    library availability, please contact Pieter de Jong
(pieterédejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Size
                                                                                                                                                                                                                                                                                                                                         Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 444 row: J column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with a combination of EcoRI and EcoRI Methylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                            The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
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1 (bases 1 to 177)
                                                                                                                                                                                                                           Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/clone="RPCI-23-444J17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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                                                                                                                                                                                                   Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Conservative
                                                                                                                                                                                                                                                                                            Tel: 301 838 0200 Fax: 301 838 0208
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Mus musculus
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                                                                REFERENCE
                                                                                        AUTHORS
                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
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/note="Vector: pT/T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
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The First Laboratory for Plant Gene Research
Kagusa DNA Research Institute
Yana 1522-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                          /clone_lib-"Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK 'Site_l: BcoRI; Site_2:
Xhoi; The cDN library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 bp mRNA linear EST 28 mi82e03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:473116 5', mRNA sequence.
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 12; DB 9; Length 177; 100.0%; Pred. No. 9.8e+03;
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/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                         /organism="Chlamydomonas reinhardtii"
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Washington University School of MedicineP
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Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                               /db_xref="taxon:3055"
                                                                                                                                                                                                                                                                                 /clone="HCL012f11_r"
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1 56 c
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Matches 12; Conservative
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Thu Aug

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 193)
Hilliar,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Rucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Riffin,L., Robhiling,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Walliamson,A., Wohldmann,P. and Wilson,R.

F., Walliamson,A., Wohldmann,P. and Wilson,R.

Contact: Wilson RK

Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 07-0CT-1996
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double-stranded cDNA was size selected, ligated to Bco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr. Minoru Ko (Mayne State University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 177.
                                                                                                                                                                                                                                                                        Gaps
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zf79f05.rl Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:383169 5', mRNA sequence.
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Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                             100.0%; Score 12; DB 9; Length 186; 100.0%; Pred. No. 1e+04; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      0; Mismatches
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/db_xref="GDB:1291426"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.Fatima Bonaldo.
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                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 12; Conservative
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                        AA074114
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Query Match 100.04; Score 12; DB 9; Length 193; Best Local Similarity 100.04; Pred. No. 1e+04; Matches 12; Conservative 0; Mismatches 0; Indels

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/Anote-Trade Corner and pawplo; Site_1: Not1; Site_2: EcoRI; 1st strand cDNA was primed with oligo(d717 on 50 mg of DNASe-treated, total cellular RNA obtained from 5,000-10 000 microdissected prenceplastic cells histologically-determined to be prostatic intrapplithelial neoplasta 2 (PIN2) cells. Obuble-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pamplo by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nih.gov
Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D.,
Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrpy/image/image.html
Seq primer: -40ml3 fwd.ET from Amersham.
                                                                                                                                                                            AA657774 1100 198 bp mRNA linear EST 05-NOV-1997 nu06f04.sl NCI_CGAP_PT2 Homo sapiens CDNA clone IMAGE:1207231, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 198)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by David Krizman."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1207231"
/clone_lib="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="45 years old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: July 31, 2002, 12:12:09
Job time: 13482 sec
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1. .198
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Best Local Similarity 100.
Matches 12; Conservative
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Unpublished (1997)
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1 caggageetega 12
                                                 69 CAGGAGCCTCGA 80
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AA657774
                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM nucleic - nucleic search, using sw model

July 31, 2002, 14:11:22; Search time 720.8 Seconds (Without alignments) 28.583 Million cell updates/sec on:

US-09-899-718A-6 12 Perfect score: ritle:

1 caggageetega 12 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1736436 segs, 858457221 residues Searched: 3472872 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1982.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:*
| SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:*
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| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1995_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1996_DAT:*
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| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999_DAT:*
| SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2000_DAT:* N_Geneseq_032802:* 112. 114. 114. 117. 119. 122. 222. 24.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001A.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2001B.DAT:*/SIDS1/gcgdata/hold-geneseg/genesegn-embl/NA2002.DAT:*

			Description		PCR primer used in	Oligonucleotide #2	Human albumin (HA)	Human albumin (HA)	Human albumin (HA)	Human bone marrow	Drosophila melanog	Human secreted pro	Eucalyptus grandis
SUMMARIES			ΙΩ		AAT63580	ABA03059	AAD22289	AAD21640	AAD20007	AAK51355	ABL27525	AAC31784	AAA69618
			80		18	22	22	22	22	22	23	21	21
		Query	Length		32	58	59	59	59	193	261	292	315
	æ	Query	Match	1 1 1 1 1 1	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	; ; ;	12	12	12	12	12	12	12	12	12
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		Result	4	:	O	υ	O	υ	υ			Ų	ပ

Human oRFX ORF1296 Human secreted pro Aloe arborescens p Secreted protein E Murine 7-transmemb Murine 7-transmemb Human Done marrow Human pecreted exp Murine 7-transmemb Murine 8-deuence Genomic sequence Genomic sequence Genomic sequence	Drosophila melanog Genomic sequence o Genomic sequence o Human CDNA sequenc DNA encoding novel EPH-like receptor Human ORFX ORF1964 DNA encoding novel
AAC75741 AAC04396 AAC04396 AAC04396 AAZ40844 AAH97774 AAH97771 AAAH97771 AAAH97771 AAAH97771 AAAH97771 AAAC33226 AAC33226 AAC32226	ABL09501 AAA57400 AAA15137 AAH1914 AAS69876 AAT02948 AAC76409
1112339991111311012222222222222222222222	22 22 23 24 25 27 27 27 27 27 27 27 27 27 27 27 27 27
344 4800 4800 4800 4800 5820 5820 6831 6831 6831 6831 1122 1122 1122 1122 1122 1122 1122 1	2674 2678 2678 2993 3107 3116 3342
	100.0 100.0 100.0 100.0 100.0
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11111111111111111111111111111111111111	8 6 4 4 4 4 4 4 4 6 0 1 2 8 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
	0 00 0

#### ALIGNMENTS

AAT63580 standard; DNA; 32 BP AAT63580; AAT63580/c RESULT

(first entry) 01-JUL-1997 

PCR primer used in CD59 minigene No. 1 construction.

Xenotransplantation; organ transplant; transgenic animal; transgenic pig; transgenic mouse; antibody mediated rejection; thyperacute rejection: ODS; complement inhibitor; primer; PCR; polymerase chain reaction; minigene; ss.

Synthetic.

WO9712035-A2

03-APR-1997.

96WO-US15255 23-SEP-1996; 96US-0675773. 03-JUL-1996; 27-SEP-1995;

(NEXT-) NEXTRAN.

Sharma A; Logan JS, Byrne GW, Diamond LE,

WPI; 1997-225881/20

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0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; neuroprotective; gene therapy; immune disorder; wound healing; hyperproliferative disorder; renal disorder; cardiovascular disorder; respiratory disorder; neurological disease; endocrine disorder; reproductive system disorder; infectious disease;
                                                                                                       A sense primer (AAT63579) and antisense primer (AAT63580) were designed to amplify a 1033 bp sequence of the 3' flanking region of the human CD59 gene, with the introduction of a 5' SacI site and 3' XhoI site. The PCR product was joined to CD59 cDMA contg. exons 3 and 4 plus 667 bp of 3' untranslated region (see also AAT63577-78)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  serum albumin; HA; antiinflammatory; immunosuppressive; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to albumin fusion proteins, which comprise
Transgenic animals expressing antigen reducing enzyme and complement inhibitor - used for production of materials suitable for human transplantation having a reduced risk of rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction) and hyperproliferative disorders
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                            to produce a CD59 minigene. This minigene was shown to retain biological function when expressed in transgenic pigs and mice. Expression of a complement inhibitor such as CD59 on endothelial
                                                                                                                                                                                                                                                  cells of transgenic animals can provide materials suitable for transplantation to humans, suppressing complement activation and
                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oligonucleotide #2 used to construct a HA fusion sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                      Example 1.1; Page 64; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 465; 606pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABA03059 standard; DNA; 58 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal disorder; ss.
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2000US-256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                         reducing immune reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rosen CA, Haseltine WA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 caggageetega 12
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200179444-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-APR-2000;
21-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA03059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABA03059,
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            In the treatment, prevention, diagnosis, and/or detection of diseases/disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g. childhood acute myeloid leukemia), arrhythmias), respiratory disorders (e.g. non-allergic finitiis), neurological diseases (e.g. Lizheimer's disease), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. measles), gastrointestinal disorders (e.g. inrealle bowel syndrome) and wound healing. In the present invention, human serum albumin (HA, see AAM52567) was used to generate fusion
  therapeutic protein and albumin. The albumin fusion proteins are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to albumin fusion proteins comprising therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; albumin; HA; fusion protein; immune system disorder; syphilis; transplant rejection; blood related disorder; myocardial infarction; hyperproliferative disorder; acute myeelold leukaemia; renal disorder; glomerulonephitis; cardiovascular disorder; arrhythmia; rhinitis; respiratory disorder; neurological disease; Alzheimer's disease; endocrine disorder; phecoytochroma; reproductive system disorder; measles; gastrointestinal disorder; irritable bowel syndrome; HIV; mumanodeficiency virus; wound healing; renal cell carcinoma; melanoma; gene therapy; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                          proteins. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                         100.0%; Score 12; DB 22; Length 58; 100.0%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                               Sequence 58 BP; 13 A; 15 C; 12 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prior CP, Turner AJ;
                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human albumin (HA) mutagenic PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodeficiency virus) or infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 190; 325pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD22289/C
ID AAD22289 standard; DNA; 59 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PRIN-) PRINCIPIA PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-APR-2000; 2000US-229358P.
25-APR-2000; 2000US-199384P.
21-DEC-2000; 2000US-256931P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      1 caggageetega 12
                                                                                                                                                                                                                                                                                                                                                                                                                                               51 CAGGAGCCTCGA 40
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                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                Matches
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protein and human albumin (HA). The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (transplant rejection); blood related disorders (myocardial infarction); hyperproliferative disorders (childhood acute myeloid leukaemia); renal disorder (glomerulonephritis); cardiovascular disorders (arrhythmias); respiratory disorders (non-allergic rhinitis); neurological diseases (Alzheimer's disorders (applinis); infections diseases (measles); gastrointestinal disorders (syphilis); infections diseases (measles); gastrointestinal disorders (srphilis); infections diseases (measles); gastrointestinal disorders (irritable bowel syndrome) and wound healing. The albumin fusion proteins are also used in the treatment of metastatic renal cell carcinoma, metastatic melanomma, malignant melanoma and HIV (human immunodeficiency virus) infection. Nucleic acid encoding albumin fusion protein is used for engineering the Xho and Cla I restriction sites into the DNA encoding HA protein in pepc0006 plasmid.

Charter The present sequence shown in sequence listing of the specification continued an ucleotide base at its 3' end.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; albumin; HA; fusion protein; therapeutic protein; vulnerary; immune system disorder; transplant rejection; blood related disorder; myocardial infarction; hyperproliferative disorder; glomerulonephritis; childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia; respiratory disorder; gene therapy; non-allergic rhinitis; nootropic; neurological disease; Alzheimer's disease; reproductive system disorder; endocrine disorder; phecoytochroma; infectious disease; antiarthritic; measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating immune system disorders (e.g. transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 12; DB 22; 100.0%; Pred. No. 8.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 59 BP; 13 A; 16 C; 12 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human albumin (HA) PCR primer #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAD21640 standard; DNA; 59 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-APR-2000; 2000US-199384P. 21-DEC-2000; 2000US-256931P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-APR-2001; 2001WO-US11924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 caggageetega 12
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                                                                                                The invention relates to albumin fusion proteins comprising therapeutic protein and human albumin (HA). Therapeutic protein fused to albumin have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. myocardial infarction), hyperproliferative disorders (e.g. childhood acute myeloid leukaemia), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhinitis), neurological diseases (e.g. Alzheimer's disease), endocrine disorders (e.g. phocytochroma), reproductive system disorders (e.g. syphilis), infectious diseases (e.g. massles), gastrointestinal disorders (e.g. irritable bowel syndrome) and wound healing. Nucleic acids encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   renal cell carcinoma; cardiovascular disorder, antimicrobial; vulnerary; arrhythmia; respiratory disorder; non-allergic rhinitis; antileukaemic; neurological disease; Alzheimer; si disease; endocrine disorder; measles; pheocytochroma; reproductive system disorder; neuroprotective; syphilis; infectious disease; gastrointestinal disorder; wound healing; nootropic; irriteable bowed syndrome; HIV; human immunodeficiency virus infection; cytostatic; antiinflammatory; gene therapy; immunosuppressive; cardiant; antianthritic; antirheumatic; renal disorder; melanoma; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                    albumin fusion protein is used in gene therapy. The present sequence is a PCR primer used for engineering the Xno and Cla I restriction sites into the DNA encoding HA protein in pPPC0006 plasmid. Note: This sequence SEQ.ID.NO.20 is stated to be similar to the
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rejection), blood related disorders (e.g. myocardial infarction) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             blood related disorder; myocardial infarction; glomerulonephritis; hyperproliferative disorder; childhood acute myeloid leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; albumin; HA; immune system disorder; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence shown in the sequence listing. However this sequence contains an additional base 'C' at the 3' end which is absent in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 59 BP; 13 A; 16 C; 12 G; 18 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the sequence shown in sequence listing.
                                                              Example 2; Page 231; 380pp; English.
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2000US-199384P.
2000US-256931P.
                    hyperproliferative disorders
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Best Local Similarity 100.
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25-APR-2000;
21-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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RESULT
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                                                                                                                                                                    corresponding netaces to disagnees. Therapeutic proteins fused to albumin or its fragments have an extended shelf-life. The albumin fusion proteins are useful in the treatment, prevention, diagnosis, and/or detection of diseases, disorders such as immune system disorders (e.g. transplant rejection), blood related disorders (e.g. childhood acute myeloid leukaemia, metastatic renal cell carcinoma, metastatic melanoma, renal cell carcinoma), renal disorders (e.g. childhood acute myeloid leukaemia, metastatic ranal cell carcinoma), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmias), respiratory disorders (e.g. non-allergic rhintis), neurological diseases (e.g. Alzheimer's diseases), endocrine disorders (e.g. pheocytochroma), reproductive system disorders (e.g. syphilis), infections diseases (e.g. measles), gastrointestinal disorders (e.g. infections diseases (e.g. measles), gastrointestinal disorders (e.g. infections diseases (e.g. measles), gastrointestinal disorders (e.g. infection and wound healing. Nucleic acids encoding albumin fusion protein is and wound healing the Arbo and Cla I restriction sites into the fusion leader sequence just 5' end of the DNA encoding the HA protein in pPPC0006 plasmid.

Note: This sequence SEQ.110 (No.20 is stated to be similar to the sequence shown in the sequence listing. However this sequence in the sequence listing. However this sequence in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                             invention relates to human albumin (HA) fusion proteins and their
                                                               Albumin fusion proteins comprising a therapeutic protein and albumin, useful in the treating metastatic renal cell carcinoma, metastatic melanoma, malignant melanoma, renal cell carcinoma, HIV (human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; bone marrow expressed exon; gene expression analysis; probe;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human bone marrow expressed single exon probe SEQ ID NO: 25912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59 BP; 13 A; 16 C; 12 G; 18 T; 0 other;
                                                                                                          immunodeficiency virus) or infection
                                                                                                                                 Example 2; Page 244; 394pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAK51355 standard; DNA; 193 BP.
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26-MAY-2000; 2000US-0207456.
30-JUN-2000; 2000US-0608408.
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Best Local Similarity 100.
            Haseltine WA;
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                                     WPI; 2001-616756/71
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            Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAK51355;
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                      Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO: 25912; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 193;
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Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                   analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the probes of the invention.
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Best Local Similarity 100.
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                                                                                                                                                                                                     Hanzel DK,
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                                                                                                                                                                                                                                                              WPI; 2001-488900/53
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                                                                                                                                                                                                        Penn SG,
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA
     222222222X8
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Sequence 261 BP; 83 A; 66 C; 68 G; 44 T; 0 other;

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Gaps
                                 ö
    Length 261;
                                Indels
100.0%; Score 12; DB 23;
100.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 0;
             Best Local Similarity 100.
Matches 12; Conservative
                                                                                   109 caggagectega 120
                                                          1 caggageetega 12
 Query Match
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expressed sequence tag; secreted protein; cDNA isolation; Human secreted protein 5' EST, SEQ ID NO: 35859. gene therapy; chromosome mapping; ss. AAC31784 standard; cDNA; 292 BP (first entry) Human; 5' EST; 06-CT-2000 AAC31784; AAC31784/C A PART OF THE PROPERTY OF THE

21-FEB-2000; 2000EP-0200610 Homo sapiens. EP1033401-A2 06-SEP-2000.

(GEST ) GENSET

99US-0122487

26-FEB-1999;

Dumas Milne Edwards J, Duclert A, Giordano J;

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures WPI; 2000-500381/45.

Claim 1; SEQ ID 35859; 71pp + CD-ROM; English

The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. expression and secretion vectors.

Sequence 292 BP; 63 A; 76 C; 73 G; 80 T; 0 other;

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                                                                                                                                                                                                   Eucalyptus grandis: Pinus radiata; modification; isoprenoid; plant; metabolism; isoprenoid blosynthetic pathway; terpenoid; steroid; genome mapping; physical mapping; postitional cloning; forestry; agriculture; medicine; fermentation; plant development; pest resistance;
                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New plant polynucleotides encoding polypeptides involved in the production and modification of isoprenoids, useful in forestry and agriculture for manipulation of isoprenoid metabolism -
                      ö
  Length 292;
                     Indels
                      ö
100.0%; Score 12; DB 21; 100.0%; Pred. No. 8.8e+02;
                     0; Mismatches
                                                                                                                                                                                Eucalyptus grandis NADPH cDNA SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
(FLET-) FLETCHER CHALLENGE FORESTS LTD.
                                                                                                                                                                                                                                             pinene; myrcene; Monterey pine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 82; 164pp; English.
                                                                                                                 AAA69618 standard; cDNA; 315 BP
                                                                                                                                                                                                                                                                                                                                                      98US-0215504.
                                                                                                                                                                                                                                                                                                                                  99WO-NZ00219.
                                                                                                                                                           (first entry)
                      Conservative
                                                      222 CAGGAGCCTCGA 211
                                          1 caggageetega 12
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-431575/37.
                                                                                                                                                                                                                                                                    Eucalyptus grandis.
          Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAB18018
                                                                                                                                                                                                                                                                                        WO200036081-A2.
                                                                                                                                                                                                                                                                                                                                 16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                    Havukkala IJ;
                                                                                                                                                                                                                                                                                                                                                     .7-DEC-1998;
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                                                                                                                                                           08-NOV-2000
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                                                                                                                                      AAA69618;
  Query Match
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The present invention describes plant polynucleotides encoding polypeptides involved in the production and modification of isoprenoids, such as terpenoid and steroid compounds. The polynucleotides are used in genome mapping, in physical mapping and in positional cloning of genes. The polynucleotides and polypeptides are useful in forestry and agriculture for manipulation of isoprenoid metabolism, in medicine for therapeutic effects, including direct application in diseased organisms or indirect application by transgenic organisms and in fermentation and chemical processing industries involving isoprenoids. In plant capplications, manipulating isoprenoid pathways or isoprenoid composition may, for example, affect plant development, pest resistance, and the value of extractives (e.g. pinene and myrcene). The ubiquitous and varied roles of isoprenoids make the polynucleotides attractive targets for blotechnical applications in a variety of fields. AAA69527 to AAA69509 and ABABB041 to ABABB143 represent Eucalyptus grandis and pluus AAA69690 and AAB18004 to AAB18143 represent Eucalyptus grandis and Pinus radiate polynucleotides and proteins used in the exemplification of the Sequence 315 BP; 77 A; 96 C; 90 G; 52 T; 0 other; invention present

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Human: open reading frame; ORFX; detection; cytostatic; hepatotropic; w vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; w vulnerary; antipsoriatic; antiparkinisonian; nootropic; neuroprotective; w anticonvolsant; costeopathic; antiarthritic; immunosuppressant; cardiant; mmunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; w hypotensive; dermatological; immunosuppressive; antidiabetic; w antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; w antianament; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; w cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; w allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; burneringe damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antidiabetic; hypotensive; dermatological; immunosippressive; antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORRX-associated disorder. The nucleic acids can be used to express ORRX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and peptides derived from open reading frame \mathbf{X}_{\prime}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
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100.0%; Score 12; DB 21; Length 315; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                      Human ORFX ORF1296 polynucleotide sequence SEQ ID NO:2591.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                             Indels
                                             0; Mismatches
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                                                                                                                                                                                                                                                      AAC75741 standard; cDNA; 341 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis; contraceptive; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0127607.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-2000; 2000WO-US08621.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0127728
                                                                                                                                                                                                                                                                                                                                           08-FEB-2001 (first entry)
                                             12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimkets RA, Leach M;
                                                                                                                                       120 CAGGAGCCTCGA 109
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                                                                                            1 caggageetega 12
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                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB41532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200058473-A2.
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                                                                                                                                                                                                                                                                                                AAC75741;
    Query Match
                                             Matches
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from RNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, astima, allegies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures –
                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                                                                                                          100.0%; Score 12; DB 21; Length 341; 100.0%; Pred. No. 8.8e+02;
                                                                                                                                                       coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                               Sequence 341 BP; 74 A; 82 C; 125 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 8471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 8471; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy; chromosome mapping; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC04396 standard; cDNA; 394 BP
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                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        267 CAGGAGCCTCGA 256
                                                                                                                                                                                                                                                                                                                                                   1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST;
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                                                                                                                                                                                                                                                               Query Match
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AAT74033 standard; cDNA; 450 BP.

AAT74033

15-SEP-1997

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AAT74033;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                     Gaps
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0
100.0%; Score 12; DB 21; Length 394; 100.0%; Pred. No. 8.8e+02; ative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human secreted protein 5' EST, SEQ ID NO: 12949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID 12949; 71pp + CD-ROM; English.
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                                                                                                                                                                                                                                                                                    AAC08974/c
ID AAC08874 standard; cDNA; 400 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                           Local Similarity 100. les 12; Conservative
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                                                                                                                                                                    117 caggagcctcga 128
                                                                                                                   1 caggageetega 12
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hes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; 5' EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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   Query Match
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Matches
                                                         Matches
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RESULT

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chromosome mapping; human; hereditary disease; diagnosis; cancer; hyperlipidaemila; oardiovascular; neurodegenerative disorder; therapy; autoimmune disease; rheumatic disease; embryogenic disorder; myopathy; renal injury; amino aciduria; hypoglycaemia; male rat infertility;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a probe for phosphoenolpyruvate carboxylase (PEPCase) from Aloe arborescens. A plasmid containing the DNA sequence of PEPCase can be introduced into a monocotyledonous plant to enhance PEPCase activity. The transformed plant has a high ability to fix carbon dioxide under dry conditions. It can also increase corn productivity when introduced into a corn plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                   Phospho:enol:pyruvate carboxylase gene of a monocotyledonous CAM plant - used to transform plants so that they can fix carbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                    PEPCase; monocotyledonous CAM plant; carbon dioxide fixation; transformation; polymerase chain reaction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 12; DB 18; Length 450; 100.0%; Pred. No. 8.8e+02; .ive 0; Mismatches 0; Indels (
                                                                                        Aloe arborescens phosphoenolpyruvate carboxylase probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Secreted protein; fingerprint identification technique;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Secreted protein EST coding sequence 78-6-2-B10-FL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 450 BP; 96 A; 101 C; 147 G; 106 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 10; 12pp; Japanese.
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ID AAZ40844 standard; DNA; 475 BP.
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Matches 12; Conservative
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                                                                                                                                                                   Aloe arborescens.
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                                                                                                                                                                                                                                                            19-0CT-1995;
                                                                                                                                                                                                                                                                                          19-OCT-1995;
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                                                                                                                                                                                                                              28-APR-1997.
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rhis sequence encodes a human secreted protein of the invention. The extended CDNAs (or genomic DNAs obtainable from them) may be used to prepare PCR primers and probes. These are useful for forensic matching or positive identification by DNA sequencing. They may also be used in alternative fingerprint identification techniques. Antibodies against the proteins encoded by the extended cDNAs are useful in identification of issue types or cell species, as well as identifying tissue specific soluble proteins. The sequences can be used for chromosome mapping and identification of genes associated with hereditary diseases or drug response. signal sequences from the cDNAs can be used in construction of secretion vectors. Other sequences derived from the extended cDNAs can be used to clone upstream genomic DNA sequences including promoters. This is in turn useful for identifying proteins that interact with promoter sequences. Some of the proteins may be useful in indagnosing and treating several disorders including, but not limited to: cancer, hyperlipidaemia, cardiovascular and neurodegenerative disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rheumatic diseases, embryogenic disorders, hypertension, renal injury, amino acidurias, hypoglycaemia, male rat infertility and myopathies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine 7-transmembrane G-protein coupled receptor coding sequence #18.
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                                                                                                                                                                                Bougueleret L, Duclert A, Dumas Milne Edwards J;
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                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 224-225; 244pp; English.
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ID AAH97774 standard; DNA; 552 BP.
                                                98US-0074121.
98US-0081563.
98US-0096116.
98US-0099273.
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            99WO-IB00282.
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                                                                                                                                                                                                                                                                                                    specific antibodies
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Best Local Similarity
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                                                                                                                                                (GEST ) GENSET
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              09-FEB-1999;
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Search completed: July 31, 2002, 14:11:24
Job time: 17381 sec
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Matches 12; Conserv
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Gaps

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Indels

100.0%; Score 12; DB 22; Length 552; 100.0%; Pred. No. 8.8e+02;

0; Mismatches

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7-transmembrane G-protein coupled protein receptors (TTM-GPCRs). The present sequence is one such murine 7TM-GPCR coding sequence. The present sequence was derived from hematopoietic stem cells. The present sequence and its corresponding protein are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate 7TM-GPCR expression. TYM-GPCRs identify specific signalling molecules, to activate an effector-signalling cascade that triggers an intracellular response and eventually a biological effect.
                                                                                                                                                                                                                                                                                             DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to murine coding sequences for
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                                                                                                                            Pereira DS;
(IMCL-) IMCLONE SYSTEMS INC.
                                                                                                                                 Lemischka IR, Witte L,
                                                 UNIV PRINCETON
                                                                                                                                                                                                                 WPI; 2001-522596/57
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279832 H.sapiens c 279864 H.sapiens c AR177408 Sequence AB020839 Homo sapi G39052 211764 Zebr

AF321195 Unculture M36196 Human synap G41958 SHGC-68982

AX349068 Sequence
AF150645 Petrotyx
AF150652 Mactacemb
AF084320 Tamarix s
G49233 DIErtcd754e
E12962 CDNA encodi

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Synthetic construct
artificial sequence.
I sites)
Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
Promoters of gene expression in plant caryopses
Patent: WO 0202785-A 6 10-JAN-2002;
Aventis CropScience GnbH (DE)
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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Sequence 6 from Patent WO0202785.
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KEYWORDS
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July 31, 2002, 14:01:53; Search time 6034.22 Seconds (without alignments) 41.616 Million cell updates/sec
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                      Compugen Ltd
                                                                                                                                                                                                                            1797656 seqs, 10463268293 residues
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         GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
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Listing first 45 summaries
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Ac066493 Glardia i Ac065036 Glardia i Ac055036 Glardia i Ac054763 Glardia i Ac054757 Glardia i Ac055110 Glardia i Ac055142 Glardia i Ac055306 Glardia i

Ac055306 Giardia i AY057834 Crocidura

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PAT 06-FEB-2002

DNA

Score

Result No.

A70150 Sequence 11 293109 M.acuminata Ac083094 Clardia 1 Ac076609 Glardia 1 Ac076609 Glardia 1 Ac085805 Glardia 1 Ac087176 Glardia 1 Ac07176 Glardia 1 Ac071714 Glardia 1 Ac07777 Glardia 1 Ac07777 Glardia 1 Ac085377 Glardia 1 Ac085377 Glardia 1 Ac043717 Glardia 1

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LOCUS G49233 442 bp mRNA linear STS 31-AUG-1999 DEFINITION DIErtd754e Mouse eight-cell stage embryo cDNA library (M. Ko) Mus
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Tamarix sp. Schultheis 19-94
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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[ (bases 1 to 258)
Schultheis, L.M. and Baldwin, B.G.
Molecular phylogenetics of Fouquieriaceae: evidence from nuclear IDNA ITS studies.
              Wiley, E.O., Johnson, G.D. and Dimmick, W.W.
Direct Submission
Submitted (12-MAY-1999) Natural History Museum, University of
Kansas, Lawrence, KS 66045, USA
                                                                                                                                                                                                                                                                                                                                                  Gaps
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Tamarix sp. Schultheis 19-94 internal transcribed spacer 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (14-AUG-1998) Integrative Biology, University of California, Berkeley, 3060 VLSB, Berkeley, CA 94720, USA Location/Qualifiers
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100.0%; Pred. No. 5.1e+03;
Live 0; Mismatches 0;
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                                                                                                                                   /specimen_voucher="KU 22982",/db_rref="taxon:94235"
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2 (bases 1 to 258)
Schultheis, L.M. and Baldwin, B.G.
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Acanthomorpha, Paracanthopterygii, Ophidiiformes, Ophidiidae,
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1 (bases 1 to 218)
Wiley, E.O., David Johnson, G. and Wheaton Dimmick, W.
The interrelationships of Acanthomorph fishes: A total evidence approach using molecular and morphological data
Biochemical systematics and ecology. 28 (4), 319-350 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                              (dases 1 to 218)
Wiley, E.O., David Johnson, G. and Wheaton Dimmick, W.
The interrelationships of Acanthomorph fishes: A total evidence approach using molecular and morphological data
Biochemical systematics and ecology. 28 (4), 319-350 (2000)
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Wiley, E.O., Johnson, G.D. and Dimmick, W.W.
Direct Submission
Submitted (12-MAY-1999) Natural History Museum, University of
                                                                                                                                                                                                                       AFIJU645 218 bp DNA linear VRI 22-AU
Petrotyx sanguineus 28S ribosomal RNA gene, partial sequence.
AFISO645
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Mastacembelus sp. 28s ribosomal RNA gene, partial sequence.
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/specimen_voucher="KU 22948"
/db_xref="taxon:94932"
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Location/Qualifiers
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KEYWORDS SOURCE

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Aloe arborescens
JP 1997107975-A/4
JP 1997107975-A/4
19-OCT-1995 JP 1995294986
SHIMADA HIROAKI, OKAMOTO TOMOKO, HONDA HIDEO, FUJIMURA TATSUTO
C12N15/09,A01H5/00,C07H21/04,C12N1/21,C12N5/10,C12N9/88, PC
                         E12962 4-JUN-1998 CDNA linear PAT 24-JUN-1998 CDNA encoding fragment of phosphoenolpyruvate carboxylase from
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1. .450
/product='Phosphoenolpyruvate carboxylase from
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H.sapiens chromosome 22 CpG island DNA genomic Msel fragment, clone
379832
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Clark, V.H., Cross, S.H., Simmen, M.W., Langford, C., Carter, N., Bickmore, W. and Bird, A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (02-SEP-1996) ICMB, University of Edinburgh, King's
Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
VCLARR@SIVO.bio.ed.ac.uk
(bases 1 to 453)
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                                                                                                                                                                     1 (bases 1 to 450)
Shimada, H., Okamoto, T., Honda, H. and Fujimura, T..
BEC-ASE GENE OF MONCCOTYLEDON CAM PLANT
Patent: JP 199710795-A 4 28-APR-1997;
MITSUI TOATSU CHEM INC

    .450
    /organism*'Aloe arborescens'

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/organism="unidentified"
/db_xref="taxon:32644"
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Chromosome 22; CpG island.
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JP 1997107975-A/4.
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/db_xref="taxon:10090"
/clone="J0521C08"
/clone_lib="Mouse eight-cell stage embryo cDNA library (M.
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                                                                               Mus musculus subvarious (Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 442)
Bergstrom, D. E., Gagnon, L. H. and Eicher, E. M. Genetic and physical mapping of the dreher locus on mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                  for 30 seconds
for 15 seconds
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for 30 seconds + 1 sec/cyc
for 10 minutes
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musculus STS cDNA clone J0521C08 3', sequence tagged site.
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                                                                                                                                                                                                                                                                 Contact: Eva M. Eicher
The Eicher Laboratory
The Jackson Laboratory
GOD Main Street, Bar Harbor, ME 04609 USA
Tel: 207/288-6344
Fax: 207/288-6077
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each 0.25 uM
each 200 uM
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Primer A: GCACTAGGGTAATCAAGGC
Primer B: ACCTGAGGTGATGTTTGGCT
STS size: 200
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2 (bases 1 to 453)

Cross, S.H., Charlton,J.A., Nan,X. and Bird,A.P.

Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P. Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (02-SEP-1996) ICMB, University of Edinburgh, King's Buildings, Mayfield Rd, Edinburgh EH9 3JR, UK. E-mail contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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Clark,V.H., Cross,S.H., Simmen,M.W., Langford,C., Carter,N.,
Bickmore,W. and Bird,A.P.
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/cell_line="lymphoblastoid"
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/clone_lib="CG122.1"
/clone="302f12"
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                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                                                                                                                                             /clone_lib="CGI22.1"
/clone="301f5"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                  148 g
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Chromosome 22; CpG island.
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Matches 12; Conservative
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Takeshita, H., Sato, M., Shiwaku, H.O., Semba, S., Sakurada, A., Hoshi, M., Hayashi, Y., Tagawa, Y., Ayabe, H. and Horli, A. Expression of the DMBT1 gene is frequently suppressed in human lung
                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear PRI 14-APR-2000
          PAT 17-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (06-DEC-1998) Akira Horii, Tohoku University School of Medicine, Department of Molecular Pathology; 2-1 Seiryo-machi, Aoba-ku, Sendai, Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp, Tel:81-22-717-8042, Fax:81-22-717-8047)
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                             1 (bases 1 to 475)
Edwards,J.-B.Dumas.Milne., Duclert,A. and Bougueleret,L.
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             linear
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             DNA
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Patent: US 6312922-A 147 06-NOV-2001;
Location/Qualifiers
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                 4,0 bp B)
Sequence 147 from patent US 6312922.
AR177408
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416. .>498
                                                             AR177408.1 GI:17919763
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Strain was digested with AluI, Cac8I, HaeIII, NlaVI, or RsaI. Fragments in the range of 250-500 bp were gel purified and a BstXI linker was added. The fragments were cloned into a modified Mlämpl9 vector and transformed into E. Coli DHSalpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide probes."
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                                                                                                                                                                                                                                                                                                                                                                                                                        BCT 24-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; environmental samples.

1 (bases 1 to 680)

Boomer, S.M., Dutton, B.E. and Lodge, D.P.

Diversity of novel green non-sulfur bacteria from Yellowstone Unpublished

2 (bases 1 to 680)

Boomer, S.M., Dutton, B.E. and Lodge, D.P.

Direct Submission

Submitted (13-NOV-2000) Dept. of Biology, Western Oregon University, 345 Monmouth, Ave., Monmouth, OR 97361, USA
                                                                                                                                                                                                                                                                         Gaps
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Uncultured bacterium rcr_15 16S ribosomal RNA gene, partial
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M36196 J05611
M36196.1 GI:338619
intrinsic membrane protein; synaptic vesicle protein 2A; synaptobrevin 1.
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/clone="rcr_15"
/country="USA: Rabbit Creek, Yellowstone"
                                                                                                                                                                        15 others
                                                                                                                                                                                                                                                                         0; Indels
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176 c 192 g 118 t
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142 g
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211764 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
G39052
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/lab_host="DH5alphaF'IQ"
/note="Vector: ml3MF19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishman@mgh.cvrc.harvard.edu
                                                          Gaps
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                        100.0%; Score 12; DB 9; Length 498; 100.0%; Pred. No. 4.7e+03;
                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primers are available from Research Genetics Inc. (http://www.resgen.com phone: 800-533-4363). Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 degrees C for 5.0 minutes
94 degrees C for 1.0 minute
58 degrees C for 1.0 minute
72 degrees C for 1.5 minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1.5 mM
50 mM
10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MJ Research PTC-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3
                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 ng
each 375 nM
each 200 uM
: 0.034 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Zebrafish AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://zebrafish.mgh.harvard.edu
Primer A: GCGACCCTTTGTGANGTTTT
Primer B: CATCTGATTGCTTTGTCCA
STS size: 297
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="AB"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mark C. Fishman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MgCL2:
                                                                                                                                                                                                                                                       G39052.1 GI:3358261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymerization:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thermal Cycler:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taq Polymerase:
Total Vol:
                                                         12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Denaturation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annealing:
                                                                                                                    176 CAGGAGCCTCGA 165
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                                                                                          1 caggageetega 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer:
                                                                                                                                                                                                                                                                                                         Danio rerio
                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dNTPs:
                                                                                                                                                                                                                                                                                        zebrafish.
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                        Query Match
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ACCESSION
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AUTHORS
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PUBMED
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JOURNAL
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                                                                                                                                                                                         G39052
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Cosmid end sequences from generated from flow-sorted chromosome 4 (Human Genome Center, Los Alamos National Laboratory), sequenced at the Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 others
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               Template: 25 ng
Primer: each 1 uM
dNTPE: each 200 uM
AmpliTaq Gold Polymerase: 0.07 units/ul
Total Vol: 5 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seymour, G.B., Bird, C.R. and Medina-Suarez, R.D. GENETIC CONTROL OF FRUIT RIPENING Patent: WO 9811228-A 11 19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 12; DB 6; L Best Local Similarity 100.0%; Pred. No. 4.4e+03; Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 12; DB 11;
100.0%; Pred. No. 4.4e+03;
Live 0; Mismatches 0;
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Sequence 11 from Patent W09811228.
A70150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="unidentified"
/db_xref="taxon:32644"
/clone="U-U55"
                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                             2.5 mM
50 mM
10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(547. .569)
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220. .569
220. .242
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Э
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Best Local Similarity 100.0
Matches 12; Conservative
                                                                                                                                                                                  Tris-HCl:
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                                                                                                                                                                                                                                                                                                                   761
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unidentified
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 Protocol:
                                                                                                                             Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind
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A70150/c
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 761)
                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 727) Archer, B.T. III, Ozcelik,T., Jahn,R., Francke,U. and Sudhof,T.C. Structures and chromosomal localizations of two human genes
                                                                                                                                                                              Draft entry and computer-readable sequence for [J. Biol. Chem. (1990) In press] kindly submitted by T.C.Sudhof, 06-JUL-1990.

Location/Qualifiers
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60 degrees C for 30 seconds
72 degrees C for 23 seconds
30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Initial incubation: 95 degrees C for 10 minutes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 12; DB 9; Length 727; Best Local Similarity 100.0%; Pred. No. 4.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                         /note="synaptobrevin 1 (SYB1); G00-125-292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perkin Elmer 9700
                                                                                                                           encoding synaptobrevins 1 and 2
J. Biol. Chem. 265 (28), 17267-17273 (1990)
91009161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="synaptobrevin 1 intron A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer A: CAGGCACAAGACTTAGCCACTT Primer B: ATGTTCTGCTTGGTTCTCTCTGTGCTCTGTGGTTCTGTGGTTCTGGTTGAC STS size: 350
                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: myers@shgc.stanford.edu
Human DNA, clone pcvP18-[1,5].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Richard M. Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Annealing:
Polymerization:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="SYB1"
                                                                                                                                                                                                                                                                                                                                                                      /gene="SYB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G41958.1 GI:3668291
                                                                                                                                                                                                                                                                                                                 /map="12p"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 4157259687
Fax: 4157259689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 caggageetega 12
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                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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                                                                                           AUTHORS
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                                                                                                              TITLE
                                                                                                                                                                                    COMMENT
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 SOURCE
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Job time: 17557 sec

Thu Aug 1 08:30:03 2002

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

July 31, 2002, 12:21:09; Search time 165.21 Seconds (without alignments) 38.657 Million cell updates/sec Run on:

US-09-899-718A-5 26

1 cccgtctaggcgttcggtgtccggcc 26 Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

Total number of hits satisfying chosen parameters:

383533 seqs, 122816752 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

Issued_Patents_NA:*

1: /cgg2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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6: /cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARTES

Result  No. Score Match Length DB ID  18.6 71.5 1248 4 US-09-105-537-7  2 18.6 71.5 1248 4 US-09-105-537-3  2 16.6 63.8 3061 1 US-08-700-576-18-6  2 16.6 63.8 15664 1 US-08-700-576-18-6  2 16.6 63.8 15664 1 US-08-700-576-18-6  2 16.6 63.8 15664 1 US-08-700-78-7  2 16.6 63.8 15664 1 US-08-700-78-7  3 16.6 63.8 15664 1 US-08-103-840-8  3 16.6 63.8 15664 1 US-08-103-840-8  4 10.0 16.4 63.1 441352 4 US-09-103-840-8  5 15 15 1392 4 US-09-103-840-8  5 15 15 1392 4 US-09-103-840-8  5 15 15 1392 4 US-09-103-840-8  5 17 1 1 16 61.5 1392 4 US-09-170-354-5  5 18 16 61.5 137 2 US-08-804-2270-7  5 18 61.5 80161 4 US-09-370-700-1  5 2 15.8 60.8 68750 4 US-09-568-102-1  5 2 15.8 60.8 68750 4 US-09-568-102-1  5 2 15.8 60.8 68750 4 US-09-568-102-1  5 2 15.8 60.8 68750 4 US-09-568-486-1  5 2 15.8 60.8 68750 4 US-09-568-486-1			dР			SUMMARIES	
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.8 60.8 68750 4 US-09	26		8.09	68750	4	US-09-568-486-1	ì
	c 27	15.8	8.09	68750	4	US-09-568-472-1	ì

Sequence 2, Appli Sequence 28, Appli Sequence 28, Appli Sequence 14, Appli Sequence 46, Appli Sequence 46, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 6, Appli	Sequence 57, Appl
US-09-443-501A-2 US-09-232-200-28 US-09-232-201-28 US-09-232-201-28 US-09-232-201-46 US-09-232-197-46 US-09-232-197-46 US-09-232-197-24 US-09-232-197-24 US-09-232-201-46 US-09-232-201-24 US-09-232-201-24 US-08-256-925-6 US-08-926-926-6 US-08-256-926-0 US-08-256-926-0 US-09-253-682-6 US-09-253-682-6 US-09-253-682-6	US-09-248-335-57
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                                                          GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin; FILE REPERENCE: 600.4380'SI; CURRENT APPLICATION NUMBER: US/09/105,537A; CURRENT FILING DATE: 1998-06-26; NUMBER OF SEQ ID NOS: 43; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.5%; Score 18.6; D
Best Local Similarity 84.0%; Pred. No. 5;
Matches 21; Conservative 0; Mismatches
                       ; Sequence 7, Application US/09105537A ; Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cccgtctaggcgttcggtgtccggc 25
                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-7
US-09-105-537-7/c
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                                                                                                                                                                                                                                                                                                                                          LENGTH:
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhae, T.
APPLICANT: Zhae, I.
TILE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REPREMENCE: 600.4380S1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT PILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 13613 Db 1068 CGCGCGAGGCGTTCGGTGTGCGC 1044 ; Sequence 3, Application US/09105537A ; Patent No. 6265202 TYPE: DNA ORGANISM: Streptomyces venezuelae ; GENERAL INFORMATION: RESULT 2 US-09-105-537-3

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Gaps ö

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63.8%; Score 16.6; DB 1; Length 3061; 82.6%; Pred. No. 41;
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LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Beyer Jr., Wayne F. TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE TITLE OF INVENTION: MYCOBACTERIUM TUBERCULOSIS COMPLEX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company
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0; Mismatches
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                    REFERENCE/DOCKET NUMBER: MOBT:024
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  748 CATCTAGGCTTTGGGTGGCCGGC 726
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; Patent No. 5476768
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ATTORNEY/AGENT INFORMATION:
NAME: FUGIL, Donna R.
REGISTRATION NUMBER: 32,135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dickson, Julie A.
Hamilton, Paul T.
Little, Michael C.
REGISTRATION NUMBER: 29,775
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                                                                               TELEFAX: 713/789-2679
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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INFORMATION FOR SEQ ID NO:
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                                                               713/787-1400
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Matches 19; Conservative
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                                                    TELEPHONE: 713/789-2679
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EDNESS: double
                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 222..425
OTHER INFORMATION:
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US-08-402-282-3/c
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APPLICANT: Steinbuchel, Alexander
AIPLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE PRODUCTION OF POLYHYDROXYALKANOATES
TITLE OF INVENTION: DNA SEQUENCE USEFUL. FOR THE PRODUCTION OF POLYHYDROXYALKANOATES
FILE REFERENCE: 11899.0024. REUSOO MOBT204-1
CURRENT APPLICATION NUMBER: US/09/570,842
PRIOR FILING DATE: 1998-05-12
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                                                               71.5%; Score 18.6; DB 4; Length 13613; 84.0%; Pred. No. 5.5; tive 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63.8%; Score 16.6; DB 1; Length 3061; 82.6%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kruger, Niels
APPLICANT: Steinbuchel, Alexander
TITLE OF INVENTION: DNA SEQUENCE USEFUL FOR THE PRODUCTION
TITLE OF INVENTION: OF POLY-3-HYDROXYALKANOATES
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
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FILING DATE: Concurrently Herewith
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                                                                                                                                                                                                   Db 11816 cgcggcgaggcgttcggtgtgcggc 11840
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                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09570842
Patent No. RE37543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 cgtctaggcgttcggtgtccggc 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: pseudomonas putida
US-09-570-842-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 19; Conservative
                                                                                                               21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity
                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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           US-09-105-537-3
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                                                                           Query Match
                                                                                                                    Matches
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OTHER INCOMMATION: frame*

NAME/REY: misc_feature

OTHER INCOMMATION: frame*

OTHER INCOMMATI
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NAME/RET. misc. feature

OTHER INPORATION: 4450.1034

OTHER INPORATION: firmme*

PRATURE: Misc. feature

CASTION: 1037.1c0366

OTHER INPORATION: firmme*

NAME/RET. misc. feature

COTHER INPORATION: firmme*

NAME/RET. misc. feature

CASTION: 1115.11786

OTHER INPORATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

CASTION: 1115.11786

OTHER INPORATION: frame*

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc. feature

OTHER INFORMATION: frame*

NAME/RET. misc. feature

NAME/RET. misc.
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COMPUTER READABLE FORM:

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LOCATION: 3731..4855
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 2747..3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 344..378
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 411.747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 1109..2014
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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                      COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTRARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/508,004
ELING DATE: 27-20L-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                        NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3283
INPORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,282
FILING DATE: 10-MAR-1995
ATTORNEY/AGBNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
MEDIUM TYPE: Floppy disk
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LOCATION: 747..1109
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; NAME/KEY: misc_feature
; LOCATION: 15429..15664
; OTHER INFORMATION: /function= "potential open reading
; OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450...10244
COTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 10371...10586
COTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: lll15.ul736
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 12748..14499
OTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 5582..574
COCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                       LOCATION: 5837..6307
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 7770.,806
CUTER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
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LOCATION: 14771..15154
                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 6403..7770
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InCATION: 8033..8236
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LOCATION: 8244..9443
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NAME/KEY: misc_feature
LOCATION: 8033.8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
NAME/KEY: misc_feature
LOCATION: 8744.9443
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OTHER INFORMATION: frame"
                                NAME/KEY: misc_feature
LOCATION: 2747.3109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 3109.3444
O'HER INFORMATION: /function= "potential open reading
O'HER INFORMATION: frame"
NAME/KE: misc_feature
LOCATION: 3444.3728
O'HER INFORMATION: /function= "potential open reading
O'HER INFORMATION: frame"
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LOCATION: 11115..11786
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5382..574
OCHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 6403..7770
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 7770..8006
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 9450..10244
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
  OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: 3731..4855
OCHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 5837..6307
OCHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 10371..10886
CHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: 4855..5376
OTHER INFORMATION: /function= "potential coding
OTHER INFORMATION: sequence"
OTHER INFORMATION: /product= "L5 gp37 homolog"
FEATURE:
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                                                 Gaps
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63.8%; Score 16.6; DB 1; Length 15664;
82.6%; Pred. No. 44;
tive 0; Mismatches 4; Indels 0;
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LOCATION: 1109..2014
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 222..425
OCHER INPORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 747..1109
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 451..747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                              ADDRESSEE: Richard J. Rodrick, Becton Dickinson and ADDRESSEE: Company STREET: 1 Becton Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,066
                                                                                                                Db 11139 CGTCCAGGATTTCGGTGTCCGTC 11117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: FUGIT, Donna R.
REGISTRATION NUMBER: 32,135
REFRENCE/DOCKET NUMBER: P-32E
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15664 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                         3 cgtctaggcgttcggtgtccggc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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LOCATION: 2034..2747
                     Best Local Similarity 82.6
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1 Becton ...
CITY: Franklin Lakes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RY: US
07417
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  Query Match
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us-09-899-718a-5.rni

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LENGTH: 1564 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 15429..15664
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                 NAME/KEY: misc_feature
LOCATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                      LOCATION: 12748..14499
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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COCATION: 14771..15134
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 15154..15456
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pearson, Robert E.
APPLICANT: Dickson, Julie A.
APPLICANT: Hamilton, Paul T.
APPLICANT: Hittle, Michael C.
TITLE OF INVENTION: MYCOBACTERIOPHAGE SPECIFIC FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Richard J. Rodrick, Becton Dickinson and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPTTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/402,068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 11139 CGTCCAGGATTTCGGTGTCCGTC 11117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REPERBNEE/CDOCKET NUMBER: P-321
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08402068 Patent No. 5633159
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STREET: 1 Becton Drive
CITY: Franklin Lakes
                                                                                                                                                 NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 3731..4855
UNTER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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                                                                                                        OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 451...747
COTHER INFORMATION: /function- "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOGATION: 747..1109
CHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /function- "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 2034..2747
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature LOCATION: 2747..3109
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LOCATION: 3444..3728
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LOCATION: 5837..6307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature LOCATION: 1109..2014
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                                                       NAME/KEY: misc_feature
LOCATION: 222..425
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, Claire M.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.8%; Score 16.6; DB 2; Length 43280; Best Local Similarity 82.6%; Pred. No. 46; Matches 19; Conservative 0; Mismatches 4; Indels 0;
APPLICANT: Sutton, Kimberly L.
TITLE OF INVENTION: POLYKETIDE SYNTHASE GENES
TIMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSER: THOMAS G. PLANT 1501
SURRET: LILLY CORPORATE CENTER
CITY: INDIANAPOLIS
                                                                                                                                                                                                                                                                                                       SOFTWARE: ASCITLES, TO SO SOFTWARE: ASCITLOS) Text only CURREWN APPLICATION DATA:
APPLICATION NUMBER: US/08/804,227C FILLING DATE: FEDELWAY 21, 1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plant, Thomas, G
REGISTRATION NUMBER: X-8231
TELECOMMUNICATION INFORMATION:
TELECHONE: 317-276-2459
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 43280 base pairs
TYPE: nucleic acid
STRANDEDEES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 27009 CGTCCAGCCGCTCGGTGTCCAGC 26987
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US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 cgtctaggcgttcggtgtccggc 25
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                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
14351..19945
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20010..31199
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36249..41774
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31232..36067
                                                                                                                                                    STATE: IN
COUNTRY: USA
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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816..14234
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LOCATION:
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LOCATION:
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; LOCATION:
US-08-804-227C-1
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
LOCATION: 10371..10586
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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NAME/KEY: misc_feature
LOCATION: 11115.11786
OTHER INFORMATION: frame"
OTHER INFORMATION: frame"
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LOCATION: 15154..1545
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                 NAME/KEY: misc_feature
LOCATION: 8033.8236
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 8244..943
OCHER INPORMATION: function= "potential open reading
OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 11917..12741
OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
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LOCATION: 14771..15154
OCHER INPORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
                  OTHER INFORMATION: /function= "potential open reading OTHER INFORMATION: frame"
                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 9450..10244
OTHER INFORMATION: function= "potential open reading
OTHER INFORMATION: frame"
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LOCATION: 12748..1449
OTHER INFORMATION: /function= "potential open reading
OTHER INFORMATION: frame"
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Patent No. 5876991
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APPLICANT: DeHoff, Bradley S.
APPLICANT: Kuhstoss, Stuart A.
APPLICANT: Rosteck, Paul R., Jr.
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7770..8006
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US-08-804-227C-1/c
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Gaps

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COMPUTER READABLE FORM:
                     MEDIUM TYPE:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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APPLICANT:
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                                                                                                                                        OTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence COTHER INFORMATION: represent a, t, c or g
93-09-103-8408-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: WINTE, Owen R.
APPLICANT: WINTE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: UPBRCUICASIS
FILE REPERENCE: 2486-24007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
UNMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63.1%; Score 16.4; DB 4; Length 4411529; 76.9%; Pred. No. 40; Live 0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                  DB 4; Length 4403765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 Jefferson Davis Highway, Fourth Floor CITY: Arlington STATE: Virginia IIP: 22202
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/07661610C
Patent No. 5292643
GENERAL INFORMATION:
APPLICANT: Toyoda, Hideyoshi
APPLICANT: Toyoda, Hideyoshi
APPLICANT: Obsta, Kazuaki
TITLE OF INVENTION: Fusaric Acid Resistant Genes
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                          9
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OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                  ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                  1 cccgtctaggcgttcggtgtccggcc 26
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Best Local Similarity 76.9%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.1%
Best Local Similarity 76.9%
Matches 20; Conservative
                     PatentIn Ver. 2.1
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                     SOFTWEEL
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4411529
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US-09-103-840A-1
                                                                               TYPE: DNA
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TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
PRIOR FILING DATE: 1997-11-25
NUMBER OF SEQ ID NOS: 437
SOFWWARE: FASTSEQ FOR WINDOWS Version 4.0
             COMPUTER: IBM PC.Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
72;
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Pred. No. 73;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5292643man F.
REGISTAATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2292-010-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16;
                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/661,610C
FILING DATE: 19910228
CLASSIFICATION: 435
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Patent No. 6355411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mahajan-Miklos, Shalina
Tan, Man-Wah
Cao, Hui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 CATCGAAACGTTCGGCGTCCGGCC 398
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0
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TELEPHONE: (703)521-4500
TELEFAX: (703)466-2347
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.5%;
79.2%;
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Goodman, Howard M.
Rahme, Laurence G.
Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 79.2'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                               LENGTH: 624 base pairs
                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown
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Best Local Similarity
Matches 19; Conserv
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US-09-199-637A-148/C
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                                        Sequence 1, Application US/08957351
Fatent No. 6306586
GENERAL INFORMATION:
APPLICANT: Semina, Elena
APPLICANT: Murray, Jeffrey C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF CATARACTS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELICT LLP
STREET: One Post Office Square
CITTLE BATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 61.5%; Score 16; DB 4; Length 1392; Best Local Similarity 79.2%; Pred. No. 74; Matches 19; Conservative 0; Mismatches 5; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08637763B
Patent No. 5849559
GENERAL INCORMATION:
APPLICANT: VAN DER WOUW, Monique J.A. et al
TITLE OF INVENTION: ARABINOXYLAN DEGRADING ENZYME
CORRESPONDENCE: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,351
FILING DATE: 24-OCT-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: ATROID() BELLE
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: UIA-024.01
TELEPHONE: 617-832-1000
TELEPHONE: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 1119 CCAGTCTAGGCGACCCCTGTCCGG 1096
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SEQUENCE CHARACTERISTICS:
LENGTH: 1392 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: CDNA US-08-957-351-1
                                                                                                                                                                                                                                                                                                                                                              02109-2170
RESULT 14
US-08-957-351-1/c
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OTHER INFORMATION: /product= "arabinoxylan degrading
OTHER INFORMATION: enzyme"
OTHER INFORMATION: /gene= "axdA"
OTHER INFORMATION: /standard_name= "arabinoxylan degrading enzyme"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,763B
FILLING DATE: 25-AUG-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MALSABIG: 29,959
REFERENCE/DOCKET NUMBER: 4615-0066.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFROE: (202) 887-1500
TELERS: 90-4030 MRSNFOERSWSH
INFORMATION FOR SEQ ID NO: 5:
ENGTH: 2101 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DAA (Genomic)
HYDORHETICAL: NOA (Genomic)
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Job time: 11850 sec
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STRAIN: CBS 120.49
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Matches 19; Conservative
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784..861
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862..1779
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LOCATION:
FEATURE:
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LOCATION:
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; LOCATION:
US-08-637-763B-5
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

July 31, 2002, 12:12:01; Search time 5855.71 Seconds (without alignments) 59:928 Million cell updates/sec Run on:

US-09-899-718A-5 26 1 cccgtctaggcgttcggtgtccggcc 26

Title: Perfect score: Sequence: Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

27472414 Total number of hits satisfying chosen parameters:

13736207 seqs, 6748477542 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

EST: *

gb_gss:*
em_gss_hum:*
em_gss_inv:*
em_gss_pin:*
em_gss_vrt:* 1: em_estba:*
2: em_esthum:*
3: em_esthu:*
4: em_esthu:*
5: em_estpu:*
7: em_estpl:*
7: em_estpl:*
1: gb_est1:*
10: gb_est2:* 9: 10: 112: 13: 15:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	BH506552 BOGFR94TF BH428842 BOGSR83TR BH391002 AG-XD-180 BM072919 MEST55-H0 BF770774 RCI-IT001 AL208141 Tetracdon A249643 IM0333K08 BM398961 5009-0-51 BB748192 601571585 AG060278 Pan trog1 BE869446 601446101 AW949999 EST31979 BG8118796 602779143 BG6118796 602779143 BG6118796 603731972 BG6118796 6037391972 B1490136 60331972 B1490136 603033972 B18867684 963093B05
SUMMARIES	BH556552 BH428842 BH321002 BH321002 BH321002 BH770774 CNSO2PLG AL46643 BH398961 BER48192 AG60278 BER69446 BER89909 BH490136 BH462300 BH40136 BH25736 BF867684
DB	110 110 110 110 110 110
% Query Match Length DB	668 747 747 700 700 711 711 711 711 1031 1031 1425 649 702 702
% Query Match	73.88 71.57 71.57 70.00 70.00 69.22 69.22 69.22 69.23 69.24 69.27 67.77
Score	19.2 19.2 18.6 18.6 18.2 18.2 18.2 18.2 19.3 10.3 17.6 17.6 17.6 17.6
Result No.	C C C C C C C C C C C C C C C C C C C

BE892849 601433981 BF241175 601880044 B1422741 603202191 B1601214 603245726 BF18048 601805281 BF770115 RC1 - FT001 BE51977 hy02b02.x AL133850 DKE2D761F BE937644 MR1-TN002 BE937644 MR1-TN002 BE937644 MR1-TN002 BE937659 MR1-TN002 BE937659 MR1-TN002 BE937644 MR1-TN002 BE937654 MR1-TN002 BE93765 MR1-TN004 B1774972 A67308 MR B1774972 A67308 MR B1774972 A67308 MR2-HT116 BG983477 PM0-CN015 BG983477 PM0-CN015 BG983477 PM0-CN015	BG747901 602705750 BG428650 602494788 BE727948 601560594 BF316519 601903032 BG281333 602401814
BEB92849 BF241175 BI662741 BI661214 BEG1214 BF180488 BI834829 BF571977 AL133850 BE937654 BE937654 BE937654 BE937654 AL22008 BE161996 BI7744972 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG992087 BG993477	
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22.22.22.22.22.22.22.22.22.22.22.22.22.	17.2
118 22222222222222222222222222222222222	44 44 45 45
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### ALIGNMENTS

	Sequence. BH506552 BH506552.1 GI:17714649 GSS.	Brassica oleracea. I Brassica oleracea Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eddicotyledons; core eudicots; Rosidae, euroside II. Parasidae, Brassidae, Brassidae	Town, C.D., Van Aken, S., Utterback, T. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001) Other_GSS: BOGFR94TR Contact: Chris Town	9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Enail: cdtcwn@tigr.cog DNA is from a doubled haploid provided by Tom Osborn. Seq prime: IF	Location delds.  Location (Journal Fiers 1. 668 / Journal Fiers 1. 668 / Journal Fiers 2. 668 / Journal Fiers 3712	genomic DNA inserted into phosi using BstXI linkers" 195 a 140 c 125 g 208 t
RESULT 1 BH506552 LOCUS DEFINITION	ACCESSION VERSION KEYWORDS	SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL COMMENT		FEATURES Source	BASE COUNT ORIGIN

a

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Direct Submission of BAC-end sequences from Anopheles gambiae
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                                                                                                                                                                                                                                                                                                                                                                                    Class: BAC ends.
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Best Local Similarity
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   TITLE
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                                                                                                                                                                                                                BH428842 12-DEC-2001 A47 bp DNA linear GSS 12-DEC-2001 BOGSZ83TR BOGS Brassica oleracea genomic clone BOGSZ83, DNA
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                             Gaps
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                                             ;
0
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   73.8%; Score 19.2; DB 12; Length 668; 87.5%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA is from a doubled haploid provided by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 own, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Drive, Rockville, MD 20850, USA.
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                                             3; Indels
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                                             0; Mismatches
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ВН428842.1 GI:17614563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cdtown@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSs: BOGSZ83TF
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1 (bases 1 to 420)
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                                               21; Conservative
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(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
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                                                                                                                                                                                                                                                                                                                                                                                                            to minimize the inclusion of DNA from microorganisms that inhabit the gut. The DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                           F.H. Collins and sequenced by The Institute for Genomic Research (TIGR). The BAC library was generated from A. gambiae PEST strain DNA. All DNA was extracted from newly hatched first instar larvae
                                                                                                                                                                                                                                                             Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Individual basecall and confidence value were assigned using the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidese; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 700)

Qiu,F., Cui,F., Guo,L., Ashlock,D.A, Wen,T.J. and Schnable,P.S.

Expressed Sequence Tags from B73 Maize Seedlings and Silks

Unpublished (2001)
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4040 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEST55-H08.T3 ISUM4-TN Zea mays cDNA clone MEST55-H08 3', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.5%; Score 18.6; DB 12; Length 420; 84.0%; Pred. No. 6.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                            Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Anopheles gambiae"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="AG-ND-180A21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Patrick S. Schnable
Schnable Laboratory
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Unpublished (2001)
Other_GSSs: AG-ND-180A21.TF
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                                                                  Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM072919.1 GI:16916614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="PEST"
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Seq primer: M13 Rev
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G. H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D. H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                          BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
                                                                     FORWARD: Forward PCR primer sequence, primer 17-1 (AA TAC GAC TCA CTA TAG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF770774
RC1-IT0013-251100-012-e09 IT0013 Homo sapiens CDNA, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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1ve 0; Mismatches 4; Indels 0
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20202663
                                                                                                                                               Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
                                                                                                                                                                                                                                                                          /clone_lib="ISUM4-TN"
/tissue_type="Seedling and silk"
/lab_host="DH10B"
                                                                                                                                                                                                                                         /db_xref="taxon:4577"
/clone="MEST55-H08"
                                                                                                                                                                                                     /organism="Zea mays"
/cultivar="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 c
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Best Local Similarity 84.09
Matches 21; Conservative
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                                                        PCR PRimers
                                  as spacers.
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VERSION
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                                                                                                                                                                FEATURES
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/clone_lib="Industriangle" //clone_lib="Industriangle" //dev_stage="Adult" //dev_stage="Adult" //note="Organ: epid_tumor; Vector: puc18; Site_l: Smal; Site_2: Smal; A mini-library was made by cloning products derived from CRESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions." 119 t
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCl&t2=RCl-IT0013-251100-012-e09&t3=2000-11-25&t4=1)
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Tetraodon nigroviridis genome survey sequence T7 end of clone
15005 of library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Terraodontidae; Tetraodontidae; Tetraodontidae; Tetraodon.

[ (bases l to 771)

Roest-Crollius, H., Jaillan, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferish Tetraodon nigroviridis
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cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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Tetraodon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                            Seq primer: puc 18 forward
High quality sequence start: 31
High quality sequence stop: 575.
Location/Qualifiers
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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AUTHORS
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KEYWORDS
SOURCE
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us-09-899-718a-5.rst

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of pWD42 (gil4732114)gblAE129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and
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Hymenostomatida; Tetrahymenina; Tetrahymena
                                                                                                                                                                                                                                                          69.2%; Score 18; DB 12; Length 319; 80.8%; Pred. No. 1e+03; Live 0; Mismatches 5; Indels
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University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       745 bp
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Best Local Similarity 80.8%
Matches 21; Conservative
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Fax: 773 702 3172
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BE748192
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dun, D., Aoyai, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AZ496643
1M0333K08F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0333K08 F, DNA sequence.
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                                                                                                           //clone_lib="G"
//note="Genoscope sequence ID : C0AG156AB03LP1-end : T7"
//note="Genoscope sequence ID : C0AG156AB03LP1-end : T7"
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                                                                                                                                                                                                                                                   70.0%; Score 18.2; DB 12; Length 771; 87.0%; Pred. No. 1e+03; tive 0; Mismatches 3; Indels 0
                                         /organism="Tetraodon nigroviridis"
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Seq primer: CGTTGTAAAACGACGGCCAGT
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Contact: Robert B. Weiss
University of Utah Genome Center
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/clone="UUGC1M0333K08"
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                                                            /db_xref="taxon:99883"
/clone="15605"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
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Matches 20; Conservative
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Fax: 801 585 7177
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be.wells linear EST 15-SEP-2000 601571585F1 NIH_MGC_55 Homo sapiens CDNA clone IMAGE:3838557 5', mRNA seminance
purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XLIO-Gold (Stratagene) cells and selected for ampicillin resistance.
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."
146 c 130 g 195 t
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EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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Direct Submission Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-Chou, Farumai-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:all.45-503-9111, Pax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 20-0CT-2000
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/clone_lib="NIH_MGC_65"
/clone_lib="NIH_MGC_65"
/tissue_type="adenocarcinoma"
/lab_host="Mgeneral"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1425)
NIH-MGC http://mgc.nci.nih.gov/.
NaH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Thoryte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 01
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/clone_lib="PTB Chimpanzee Male BAC Library"
227 c 400 g 262 t 39 others
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80.8%; Pred. No. 1.3e+03;
"wismatches 5; Indels
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/db_xref="taxon:9598"
/clone="PTB-047L15.F"
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/db_xref="taxon:9606"
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R.Site 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="from acute myelogenous leukemia"
/lab.host="DH100 (T1 phage-resistant)"
/lab.host="DH100 (T1 phage-resistant)"
/note="Organ: bone marrow; Vector: pDNR-LIB (Clontech);
Site_1: Sili (ggcgctcggcc); Site_2: Sili (ggccattatggcc); Site_1: Sili (ggcgctcggcc); Site_2: Sili (ggccattatggcc);
Site_1: Sili (ggcgctcggcc); Site_2: Sili (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA.
5, adaptors were used in cloning as follows: 5,
adaptors sequence: 5,-CACGGCCATATGGCC.3 and 3, adaptor
sequence: 5,-ATTCTAAAGGCCGAGCGCGACATG-dT(30)BN-3,
(Where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.65 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA).

80 a 260 c 232 g 172 t) to thers
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GSS; GSS (genome survey sequence).

Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male

BAC Library clone:PTB-047L15.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 03-NOV-2001
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Pan troglodytes DNA, clone: PTB-047L15.F, genomic survey sequence.
AG060278
                                                                            Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 845)
MIH-MCO http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: They denomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T. Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
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69.2%; Score 18; DB 10; Length 845;
Best Local Similarity 80.8%; Pred. No. 1.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:3838557"
/clone_lib="NIH_MGC_55"
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Location/Qualifiers
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|| || || || || || || || || || || || 673 CCGTCAAGCCGCTCGGTGTCCCGCC 648
BE748192.1 GI:10162184
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van der Hoeven, R.S., Bezzeredes, J.L., Matern, A.L., Holt, I.E., Liang, F., Hansen, T., Craven, M.B., Bowman, C.L., Ronning, C.M., Nierman, W., Fraser, C.M., Martin, G.B., Giovannoni, J.J. and Tanksley, S.D. Generation of ESTs from tomato flower tissue, 0-3 mm buds
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="tomato flower buds 0-3 mm, Cornell University"
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM10822 row: e column: 11
High quality sequence stop: 432.
Lication/Qualifiers
Location/Qualifiers
Location/Qualifiers
Location/Colabiliers
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: brain; Vector: pCNV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:4914802"
/clone_lib="NCL_CGAP_Brn67"
/tissue_type="anaplastic oligodendroglioma with lp/19q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE462300 499 bp mRNA linear EST 18-N
EST324564 tomato flower buds 0-3 mm, Cornell University
Lycopersicon esculentum cDNA clone cTOA12G14, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 17.6; DB 10; Length 495;
Pred. No. 1.7e+03;
0; Mismatches 4; Indels 0
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (Tl phage-resistant)"
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/cultivar="TA496"
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/clone="cTOA12G14"
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BE462300.1 GI:9508069
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83.38;
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Best Local Similarity
Matches 20; Conserv
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602779143F2 NCI_CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4914802
5', mRNA sequence.
BG818796
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1 (bases 1 to 633)

Hegde, P., Qi,R.; Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
         Library constructed by Life
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

Unpublished (2000)

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Fal: 301 838 3528

Fax: 301 838 0208

Email: johnq@tigr.org
                                                                                                                                                                                    Gaps
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                                                                                                                                       Score 18; DB 10;
Pred. No. 1.4e+03;
0; Mismatches 5;
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/db_xref="taxon:9606"
/db_wref="MAGE resequences,
/note="Vector: pBluescriptSKm"
      Average insert size 1.8 kb.
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                                Technologies.
                                                                                                                                         69.2%;
80.8%;
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Matches 21; Conservative
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Best Local Similarity
Matches 19; Conserv
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Gaps

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EST 18-MAY-2001

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//note="Organ: pooled brain, lung, testis; Vector:
//note="Organ: pooled brain, lung, testis; Vector:
pcWW-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1:8 kb,
insert size range 1:3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B1490136 591 bp mRNA linear EST 28-AUG-2001 603031972F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5173480 5',
                                                                                                                                                                                                                                                                                                                                                                              ö
/tissue_type="flower"
/dev_stage="0-3mm buds"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; supplier: Tankalay; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
column: 17
High quality sequence stop: 591.
Location/Qualifiers
I..591
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:517480"
                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                    Query Match 67.7%; Score 17.6; DB 10; Length 499; Best Local Similarity 83.3%; Pred. No. 1.7e+03; Matches 20; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NIH_MGC_115"
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Gaps

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1 cccgtctaggcgttcggtgtccgg 24

20; Conservative

Matches

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58 CCCGACGATGCGCTCGGTGTCCGG
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Search completed: July 31, 2002, 12:12:05 Job time: 13478 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

July 31, 2002, 14:11:17; Search time 720.8 Seconds (without alignments) 61.931 Million cell updates/sec Run on:

1 cccgtctaggcgttcggtgtccggcc 26 US-09-899-718A-5 26 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1736436 seqs, 858457221 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database :

N_Geneseq_032802:*

N_correseq_uscator_incld_geneseq_geneseqn-embl/NA1980.DAT:*

| SIDSI/gcgdata/hold-geneseq_geneseqn-embl/NA1981.DAT:*
| SIDSI/gcgdata/hold-geneseq_geneseqn-embl/NA1991.DAT:*
| SIDSI/gcgdata/hold-geneseq_geneseqn-embl/NA20018.DAT:*
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| SIDSI/gcgdata/hold-geneseq_geneseqn-embl/NA20018.DAT:* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	S. venezuelae deso	S. venezuelae deso	S. venezuelae deso	Micromonospora med	Human pentraxin I	Human breast cell	Human foetal liver	Probe #4686 for de	Human brain expres
		ID		AAZ87284	AAZ87319	AAF30757	AAH41415	ABA46067	ABA56605	ABA26220	AAK04749
		BB	21	21	21	22	22	22	22	22	22
		re Match Length DB I	1248	12441	13613	47981	1680	381	381	381	381
æ	Query	Match	71.5	71.5	71.5	67.7	66.2	65.4	65.4	65.4	65.4
		Score	18.6	18.6	18.6	17.6	17.2	17	17	17	17
	lt.	No.	-	7	ო	4	S	9	7	œ	6
	Result	- !	ပ			O	O	O	O	υ	O

Human bone marrow	Probe #4804 for ge	Probe #4913 used t	Probe #4649 used t	Polycistronic oper	Human colon cancer	Human reproductive	Human secreted pro	Nucleotide sequenc	G. oxydans autonom	Mycobacteriophage	Mycobacteriophage	Mycobacteriophage	Nhel-G/Spel fragme	Tylactone synthase	Drosophila melanog	Human secreted pro	Human nervous syst	Human nervous syst	Drosophila melanog	Drosophila melanog	Mycobacterium tube	Prepro-polygalactu	Human cDNA encodin	Quorum sensing con		Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila melanog	Mycobacterium tube	Mycobacterium tube	Human digestive sy	Human liver associ	_	Drosophila melanog
AAK30275	AAI14871	AAI36227	AAI04658	AAQ06685	AAH35021	AAL04931	AAC12097	AAV22799	AAX57803	AAT09312	AAT70492	AAT66130	AAT51224	AAT80413	ABL27597	AAF22378	ABA16862	ABA19759	ABL06699	ABL18703	AAS03788	AAQ11271	AAF93794	AAF77899	ABL07609	ABL06698	ABL18702	ABL07608	K			<	AAS31795	AAF30761	ABL25667
22	22	22	22	11	22	22	21	19	20	17	18	18	18	18	23	21	22	22	23	23	22	12	22	22	23	23	23	23	23	22	22	22	22	22	23
381	381	381	381	1463	2443	32249	120	3061	4599	15664	15664	15664	15664	43280	952	1175	1343	1343	1571	1959	2310	2495	2547	3090	3442	3728	4109	12713	24221	4403765	4411529	303	303	528	280
55.4	65.4	.,	u ı	ഗ		65.4	$\epsilon$	$\epsilon$	3	63.8	$^{\circ}$	$\sim$	3	Э.	ж.	63.1	ж,	3.	3.	63.1	3	ж.		Э.	3		Э.	ж,	З,	ж.	÷.	2	62.3		52.3
17 (	7	_			7	17	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	6.4	16.4	6.4	6.4	6.4	6.4	6.4	4.	6.4	6.4	٠4	6.4	6.4	4.	6.4	6.4	6.4	6.2	16.2	6.2	9
10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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#### ALIGNMENTS

RESULT

AAZ87286/c ID AAZ87286 standard; DNA; 1248 BP.

AAZ87286; 

(first entry) 05-JUN-2000 S. venezuelae desosamine biosynthetic gene desI, SEQ ID NO:7.

Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.

Streptomyces venezuelae ATCC15439

Location/Qualifiers 1..1248 /*tag= a /*tag= a /product= "DesI"

WO200000620-A2

06-JAN-2000

99WO-US14398. 25-JUN-1999; 98US-0105537. 26-JUN-1998;

(MINU ) UNIV MINNESOTA

Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.

synthesis of methymycin and pikromycin Claim 2; Page 281-287; 438pp; English.

Sherman DH, Liu H, Xue Y, Zhao L;

WPI; 2000-160679/14.

P-PSDB; AAY77179

(MINU ) UNIV MINNESOTA.

98US-0105537. 99WO-US14398.

25-JUN-1999; 26-JUN-1998;

Page

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cholesterol lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well sulfing insecticides) via expression of polyketides in plants. Sequences AAB7286-287294 represent desosamine biosynthetic genes from streptomyces venezuelae ATCC 15439, which encode proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                           production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methywycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics,
                                                                                                                                                                                                                    The invention relates to an isolated and purified nucleic acid segment comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the eryC gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pixromycin, neomethymycin, narbomycin or a combination of these compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the
                                                                                                                     Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S. venezuelae desosamine biosynthetic gene cluster pikB, SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1248 BP; 177 A; 546 C; 377 G; 148 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                           synthesis of methymycin and pikromycin
                                                                                                                                                                                 Claim 3; Page 353-354; 438pp; English.
                 Xue Y, Zhao L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ87284 standard; DNA; 12441 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.5%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.59
Best Local Similarity 84.09
Matches 21; Conservative
                                                       WPI; 2000-160679/14.
              Liu H,
                                                                                 P-PSDB; AAY77181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY77181-Y77189
                   Sherman DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ87284;
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AAZ87319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiocil; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmorary disease; respiratory inflammation; hypercholesterolaemia; crop protection agent; ds.
                                                                Gaps
Score 18.6; DB 21; Length 1248; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces venezuelae ATCC15439
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06-JAN-2000.

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as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemotherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are useful for synthesis of methymycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyalkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                            Internation relates to an instance and purified material segment comprising a descamine blosynthetic gene cluster, a fragment of its biologically active variant, where the nucleic acid sequence is not derived from the eryc gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide pixtomycin, neomethymycin, narbomycin or a combination of these pixromycin, necephance cluster encodes proteins which synthesise methymycin, pompounds. Recombinant or a ungmented cells comprising the descamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungicides or insecticides) via expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Desosamine biosynthesis; macrolide; polyketide; methymycin; pikromycin; neomethymycin; narbomycin; polyhydroxyalkanoate monomer synthase; biopolymer; antibiotic; chemotherapeutic; immunosuppressant; asthma, chronic obstructive pulmonary disease; respiratory inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated and purified nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polyketides in plants. The present sequence represents the desosamine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biosynthetic gene cluster from Streptomyces venezuelae ATCC 15439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.5%; Score 18.6; DB 21; Length 12441; 84.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacteria, including multi-drug resistant pneumococci and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12441 BP; 1704 A; 4294 C; 4686 G; 1757 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 cccgtctaggcgttcggtgtccggc 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ87319 standard; DNA; 13613 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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Best Local Similarity
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/product= "pikB gene cluster protein #6 (AAY77208)"
/note= "No termination codon given in the specification"
/transl_except= (pos:8273.0.8275, aa:Ynt)
/transl_except= (pos:8275.8275, aa:Thr)
/transl_except= (pos:8276.8278, aa:Gly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprising a desosamine biosynthetic gene cluster, a fragment or its biologically active variant, where the nucleic acid sequence is not derived from the erry gene cluster of Saccharopolyspora erythraea or Streptomyces antibioticus. The invention also relates to a macrolide biosynthetic gene cluster, or fragments thereof. The macrolide biosynthetic gene cluster encodes proteins which synthesise methymycin, pikromycin, neomethymycin, narbomycin or a combination of these
                                                                   product= "PikB gene cluster protein #1 (AAY77204)"
/note= "No initiation codon given in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated and purified nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Desosamine and macrolide biosynthetic gene clusters, useful for, e .g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY77204, AAY77205, AAY77206, AAY77207, AAY77207, AAX77209, AAY77210, AAY77211, AAY77212, AAX80999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "PikB gene cluster protein #10 (AAY77211)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "PikB gene cluster protein #11 (AAY77212)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "PikB gene cluster protein #9 (AAY77210)"
complement (13706..15043)
                                                                                                                             product= "PikB gene cluster protein #2 (AAY80998)"
                                                                                                                                                                                                                  /product= "PikB gene cluster protein #4 (AAY77206)"
/transl_except= (pos:6837..6841, aa:Gln)
7492..8205
                                                                                                                                                                                                                                                                         /product= "PikB gene cluster protein #5 (AAY77207)"
complement (7942..8205)
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="PikB gene cluster protein #7 (AAY80999)"
complement (11271..12149)
                                                                                                                                                              *tag= c
product= "PikB gene cluster protein #3 (AAY77205)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "PikB gene cluster protein #8 (AAY77209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (12342..13799)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                synthesis of methymycin and pikromycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Figure 32; 438pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhao L;
            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15404..15574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu H, Xue Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US14398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0105537
                                                                                                                                             ..6741
                                                                                                                                                                                       6834..7402
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                                                                                                .2014
                                                        /partial
                                                                                                                                                                                                                                                                                                         'partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherman DH,
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compounds. Recombinant or augmented cells comprising the desosamine and/or macrolide biosynthetic gene clusters are useful for the production of biologically active macrolides. The macrolide biosynthetic proteins are useful for synthesis of methywycin, pikromycin, neomethymycin and narbomycin. The alternative termination of polyketide synthesis may be useful to prepare novel antibiotics and polyhydroxyatkanoate (PHA) monomers. The compounds produced by the recombinant host cells are useful as biopolymers, e.g., in packaging or biomedical applications, to engineer PHA monomer synthases or to prepare biologically active agents, such as chemortherapeutics, immunosuppressants, agents to treat asthma, chronic obstructive pulmonary disease as well as other diseases involving respiratory inflammation, cholesterol-lowering agents or macrolide-based antibiotics which are active against a variety of organisms, e.g., bacteria, including multi-drug resistant pneumococci and other respiratory pathogens, as well as viral parasitic pathogens, or as crop protection agents (e.g., fungleides or insecticides) via expression of polyketides in plants. The present sequence represents the desosamine biosynthetic gene cluster (pik) from Streptomyces venezuelae ATCC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "TDP-4-keto-6-deoxyhexose 3,4-isomerase"
/hote= "encodes AAB82202"
2072..3382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Micromonospora megalomicea megalomicin biosynthetic gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; Length 13613;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "TDP-megosamine glycosyltransferase"
/note= "eryCIII homologue; encodes AAB802203"
                                                                                                                                                                                                                                                                                                                                                   Sequence 13613 BP; 1858 A; 4733 C; 5092 G; 1930 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Megalomicin; meg gene; polyketide synthase; antibiotic;
motilide; antiparasitic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "mycarose O-acyltransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="TDP-4-keto-6-deoxyglucose-
2,3-dehydratase"
                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
                                                                                                                                                                                                                                                                                                                                                                                                   71.5%; Score 18.6; Interity 84.0%; Pred. No. 31; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "encodes AAB82201"
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/product= "mycalcoll"
/morte= "encodes AAB82204"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 11816 cgcggcgaggcgttcggtgtgcggc 11840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF30757 standard; DNA; 47981 BP.
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/qene= "meqDVI"
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/gene= "megDII"
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/gene= "megY"
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                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
hes 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUN-2001
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Matches
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    /*tag= k
/gene = "megBLV"
/product= "npp-4-keto-6-deoxyhexose 4-ketoreductase"
/note= "encodes AAB82211"
                                                                                                                                                          /product= "TDP-4-keto-6-deoxyhexose 4-ketoreductase"
/note= "eryVIV, dnmV homolgoue; encodes AAB82208"
complement (8228..9220)
                                                                                      /*tag= g
/gene= "megDIV"
/product= "TDP-4-keto-6-deoxyhexose 3,5-epimerase"
/honce= "eryBVIII, dnmU homologue, encodes AAB82207"
7220..8206
                                                                                                                                                                                               /gene= "megBII-1(megDVII)"
/groduct= "TDP-4-keto-6-deoxyhexose 2,3-reductase"
/note= "encodes AAB82209"
complement (9226..10479)
                                     /*tag= f
/gene= "megDIII"
/product= "daunosaminyl-N,N-dimethyltransferase"
/product= "eryCVI homologue; encodes AABB2206"
6592..7197
                 /note= "eryCI, DnrJ homologue, encodes AAB82205"
5822..6595
                                                                                                                                                                                                                                                                                                                                                                          note- "polyketide synthase; encodes AABB2212" (2505..13470
                                                                                                                                                                                                                                                                                                                                                             /product= "megalomicin 6-deoxyerthronolide B synthase 1"
                                                                                                                                                                                                                                                            /product= "TDP-mycarose glycosyltransferase"
/note= "encodes AAB82210"
complement (10483..11424)
'product= "TDP-3-keto-6-deoxyhexose
           3-aminotransaminase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene= "megA"
/function= "ACP-L"
13849..15126
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/gene= "megA"
____ion= "KS1"
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"megA"
- "AT1"
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/gene= "megA"
/function= "KR1"
17947..18207
                                                                                                                                                                                                                                                                                                                                                                                                                      "AT-L"
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/function= "KS2"
19876..20910
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                                                                                                                                        /*tag= h
/gene= "megDV"
                                                                                                                                                                                                                                           /*tag= j
/gene= "megBV"
                                                                                                                                                                                                                                                                                                                                          'gene= "megA"
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gene= "megA"
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gene= "megA"
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21517..22053
/*tag= u
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3576..13791
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5427..16476
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8268..19548
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Synthase 2" vecayerythronolide B
/note= "polyketide synthase, encodes AAB82213"
22957..24237
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/gene= "megalomicin 6-deoxyerythronolide B
/product= "megalomicin 6-deoxyerythronolide B
synthase 3"
/note= "polyketide synthase; encodes AAB82214"
22957..24237
                                                                                                                                                                                                                                                                                     /*tag= z
/gene= "megAII"
/function= "KR3 (inactive)"
26998..2258
                                                                                                                                                                                                                                                                                                                                         /*tag= aa
/gene= "megAII"
/function= "ACP3"
27393.28590
/*tag= ab
/gene= "megAII"
/function= "KS4"
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/*tag= ae
/gene= "megAII"
/gene= "ER4"
                                                                                                                                                                                                                          /*tag= y
/gene= "megAII"
-+ion= "AT3"
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/*tag= ad
/gene= "megAII"
/con= "DH4"
                                                /gene= "megA"
/function= "ACP2"
                                                                                                                                                                              /*tag= x
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/function= "KS3"
24544..25581
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/gene= "megAII"
/function= "AT4"
29953.30477
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/gene= "megAIII"
/function= "KS5"
24544..25581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          function= "ACP4"
3666..43271
/gene= "megA"
/function= "KR2"
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'function= "KR4"
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/gene= "megAIII"
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/gene= "megAIII"
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26230..26733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= ak
/gene= "megAIII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= ag
/gene= "megAII"
                                                                                                         /gene= "megAII"
                       22318..22575
                                                                             22867..33555
                                                                                                                                                                                                                                                              /function= "A
26230..26733
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28897..29931
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31396..32244
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32257..32799
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                                                                                                                                                                                                                                                                                                                                                                                         Human; pentraxin I; pentraxin receptor; neuronal disorder; inhibitor; detection; neuroprotective; nootropic; cerebroprotective; cytostatic; gene therapy; acute head trauma; multiple sclerosis; spinal cord injury; Alzheimer's disease; brain Lumour; stroke; neuroprotective; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding the human Pentraxin receptor useful for preventing, treating, ameliorating or detecting a disease associated with a neuronal disorder such as a stroke, multiple sclerosis, or
                                                                                                                                                                                              Gaps
                                                                                                                                                                      Length 47981;
                                                                                                                                                                                             ;
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Rodes Gubern B, Adan Plana J, Puig CN, Carceller RA;
Masa Alvarez M, Piulats X, Den Daas I, Trullas OR;
DeGregorio-Rocasolano BN;
                                                                                                                                                                                              Indels
                                                                                                                                                                      DB 22;
                                                                                                                                                                                             4;
                                                                                                                                                                                                                                                                                                                                                                     Human pentraxin I encoding cDNA SEQ ID NO:1.
                                                                                                                                                                                             Mismatches
                                                                                                                                                                      Score 17.6;
                                                                                                                                                                                                                   Pred.
                                 /function= "KS6"
28897..29931
/*tag= an
/gene= "megAIII"
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                                                                            "AT6"
                                                                                                               'gene= "megAIII"
                                                                                                                                                                                                                                                                                                AAH41415 standard; cDNA; 1680 BP
                      "megAIII"
                                                                                                                                                                                             ;
0
                                                                                 /function="KF
31396..32244
/*tag= ap
27393..28590
                                                                                                                                                                      67.7%;
83.3%;
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                                                                             /function=
29953..3047
                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                             Conservative
             /*tag=
                       gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-357928/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease
                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-NOV-1999;
 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP1101820-A1
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                                                                                                                                      misc_feature
                                            misc_feature
                                                                                           misc_feature
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                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                        AAH41415;
                                                                                                                                                                       Query Match
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                                                                                                                                                                                              Matches
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pentraxin receptor (hpr) or a protein exhibiting biological properties of hpr and having a sequence selected from: (a) a fully defined 1853 bp sequence given in AHH1416; (b) a sequence which hybridises with (a); (c) a degenerate variant which deviates from (a) or (b); and (d) a fragment, derivative or allelic variation of (a), (b) or (c). (I) has neuroprotective, nootropic, cerebroprotective and cytostatic activity,

The present invention describes a nucleic acid (I) encoding the human

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and can be used in gene therapy. Pentraxin I, hPr, or hPr-encoding sequences are useful in the preparation of pharmaceutical compositions for preventing, treating or ameliorating a disease associated with a neuronal disorder such as stroke, acute head trauma, multiple sclerosis, spinal cord injury, Alzheimer's disease or brain tumour, or for providing a neuroprotective effect. The present sequence represents the human cDNA coding sequence of pentraxin I, which is used in an example from the present invention.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes -
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                                                                                                                                                                                                                            Score 17.2; DB 22; Length 1680; Pred. No. 1.3e+02; 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 4762; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human breast cell single exon nucleic acid probe #4762.
                                                                                                                                                                            Sequence 1680 BP; 328 A; 571 C; 526 G; 255 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanzel DK, Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                 519 CGTCTCGGCGGCCGGTGTCCGG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                               ABA46067 standard; DNA; 381 BP.
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                                                                                                                                                                                                                                                                                                              3 cgtctaggcgttcggtgtccgg 24
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2000US-0207456.
2000US-0608408.
                                                                                                                                                                                                                                  66.2%;
86.4%;
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21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                              Query Match 66.2°
Best Local Similarity 86.4
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease; cancer; ss.
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03-AUG-2000;
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Indels

Pred. No. 1.5e+02; ); Mismatches 5;

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Conservative

80.08;

Best Local Similarity

20;

Matches

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diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                     65.4%; Score 17; DB 22; Length 381; 80.0%; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #4910.
                                                                                                                                                                                                                                         Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                     Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 CGGCGAGCGTTCAGAGTCCGGCC 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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2000US-0608408.
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27-SEP-2000; 2000US-0236359.
04-OCT-2000; 2000GB-0024263.
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30-JUN-2000;
03-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
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65.4%; Score 17; DB 22; Length 381;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Single exon nucleic acid probes for analyzing gene expression in human
   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                       Probe #4686 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                       Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia;
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80.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences.
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                                                  241 CGGCCGAGGCGTTCAGAGTCCGGCC 217
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                            2 cogtetaggegtteggtgteeggee 26
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                                                                                                                                         ABA26220 standard; DNA; 381 BP
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                                                                                                                                                                                                                                                                                                       congenital heart disease; ss.
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2000US-0608408.
2000US-0632366.
2000US-0234687.
2000US-0236359.
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21-SEP-2000; 2000US-0234687
27-SEP-2000; 2000US-0236359
04-OCT-2000; 2000GB-0024263
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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30-JUN-2000;
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microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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2000US-0207456.
2000US-0608408.
2000US-0632366.
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Best Local Similarity 80.0
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cervical cancer; ss
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                                        WO200157276-A2.
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30-JUN-2000; 2
03-AUG-2000; 2
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                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                             Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
                                                                                                                 Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.4%; Score 17; DB 22; Length 381;
80.0%; Pred. No. 1.5e+02;
tive 0; Mismatches 5; Indels
                                                                                             Human brain expressed single exon probe SEQ ID NO: 4740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 CGGCGAGGCGTTCAGAGTCCGGCC 217
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                                AAK04749 standard; DNA; 381 BP
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2000US-0234687.
2000US-0236359.
2000GB-0024263.
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2000US-0608408
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                                                                        05-NOV-2001 (first entry)
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Matches 20; Conservative
                                                                                                                                       epilepsy; cancer; ss
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21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                        26-MAY-2000;
30-JUN-2000;
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                                                                                                                                                                                                    09-AUG-2001
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                                                     AAK04749;
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                      AAK04749/C
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            RESULT
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probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analyzing gene expression in human bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                             Rank DR;
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                                                            04-FEB-2000, 2000US-0180312.
26-MAY-2000, 2000US-0207456.
30-UUN-2000; 2000US-0603408.
03-AUG-2000; 2000US-0532366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0224263.
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30-JAN-2001; 2001WO-US00668
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Gaps

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Human genome-derived single exon nucleic acid probes useful for
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                                                                                                                                                        The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hela cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probe #4913 used to measure gene expression in human placenta sample.
                                                                                                        Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                     analyzing gene expression in human cervical epithelial cells -
                                                                                                                                                                                                                                                                                                              Length 381;
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Best Local Similarity 80.0%; Pred. No. 1.5e+02;
0: Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                             Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                          at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                        Claim 25; SEQ ID No 4804; 487pp; English
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                                                               Hanzel DK, Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                 241 CGGCGAGGCGTTCAGAGTCCGGCC 217
                                                                                                                                                                                                                                                                                                                                                      2 ccgtctaggcgttcggtgtccggcc 26
                                          (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0207456.
2000US-0608408.
2000US-0532366.
2000US-0234687.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0236359.
                      2000GB-0024263.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic disorder; ss.
                                                                                    WPI; 2001-488901/53.
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03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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                      04-OCT-2000;
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                                                                Penn SG,
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The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe breast. The probes are useful for a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human breast particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases of the breast, fibrocystic changes, proliferative breast disease and
                                                                                                                                     The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probe, human, breast disease, breast cancer, development disorder; ss, inflammatory disease; proliferative breast disease; non-carcinoma tumour.
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                                                                                                                                                                                                                                                                               for antenatal diagnosis of human genetic disorders.
                                                                                                                                                                                                                                                                                                                                                         Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
analyzing gene expression in human placenta
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                                                           Claim 25; SEQ ID No 4913; 654pp; English.
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30-UUN-2000; 2000US-0608408,
03-AUG-2000; 2000US-0632366,
21-SEP-2000; 2000US-0234687,
27-SEP-2000; 2000US-02368399,
04-OCT-2000; 200GS-0024263,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Hoffman SJ,
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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                           Gaps
                                                                                                                                                            Polycistronic operon for coexpression of (des-Val)-alpha-(Gly-Gly)-alpha globin and des-Val beta globin.
                                                                                                                                                                                 Polycistronic operon; di-alpha-globin; di-beta globin; haemoglobin;
                                                                                                                                                                                                                                                         product=(des-Val)-alpha-(Gly-Gly)-alpha globin
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                                            65.4%; Score 17; DB 22; Length 381;
80.0%; Pred. No. 1.5e+02;
Live 0; Mismatches 5; Indels
                          Sequence 381 BP; 92 A; 130 C; 95 G; 64 T; 0 other;
                                                                                                                                                                                                                                                                                                      product=(des-Val)-alpha globin
                                                                                                                                                                                                                                                               190..1012
/label=cotranslational coupler
                                                                                                                                                                                                                                     'label=cotranslational coupler
                                                                                                                                                                                                                                                                            .019..1457
/label=des-Val beta globin
                                                                                                                                                                                                                                                                                                                          product=Gly-Gly linker
                                                                                                                                                                                                                                                                                                                                             product=alpha globin
                                                                                                                                                                                                                 Location/Qualifiers
                                                                       BP
                                                                                                                     AAQ06685 standard; DNA; 1463
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89US-0374161.
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1005..1012
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72..77
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                                             Query Match 65.4%
Best Local Similarity 80.0%
Matches 20; Conservative
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976..980
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                                                                                                                                                                                                     synthetic
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                                                                                                               AAQ06685
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Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
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                                                                                                                                                                                                                                                                                                                                                          This polycistronic operon contains the di-alpha and beta-globin genes in separate cistrons, both preceded by a short cotranslational coupler region. The di-alpha-globin gene is transcribed first as it affects folding of the beta globin. This is essential for incorporation of the haem molecule to form functional haemoglobin. The 2 alpha-like polypeptides encoded are nearly identical and sepd. by an interposed Gly-Gly linker. The synthetic haemoglobin produced on transformation of host, eg. yeast, cells has an increased intravascular half life. The 5' end overhangs the 3' end of the complementary strand by AATT and the 5' end of the complementary strand by AATT and this sense strand by TCGA. See also AAQ06684.
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                                                                                                                                                             Di-alpha and di-beta globin-like polypeptide(s) - used for prodn. of haemoglobin having increased half-life and produced in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon cancer; colon cancer antigen; diagnosis; detection;
Stetler GL, Wagenbach M;
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   Looker DL, Rosendal MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 ccgtcgtggtgttctgtctccggcc 532
                                                                                                                                                                                                                                                                                                      Disclosure; fig 12; 22pp; English.
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Matches 20; Conservative
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P-PSDB; AAG75616.
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03-NOV-1999;
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CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
Cd diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC in a patient's genome that affect the activity of P by expressing
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patients own production of P.
CC diactive proteins or to supplement the patients own production of P.
CC by inserting the nucleic acids into a host cell and culturing the cell
CC express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB377789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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2 cogtctaggcgttcggtgtccggcc 26 ||| ||| ||| ||| |||| ||||| ||||| 130 ccgmctagccgtgcggtgccaggcc 154 Ω δλ

Query Match 65.4%; Score 17; DB 22; Length 24 Best Local Similarity 80.0%; Pred. No. 1.6e+02; Matches 20; Conservative 0; Mismatches 5; Indels

ó;

Gaps ;

Length 2443;

Search completed: July 31, 2002, 14:11:22 Job time: 17379 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Description

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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100.0%; Score 26; DB 6; Length 26; 100.0%; Pred. No. 0.53; cive 0; Mismatches 0; Indels
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Aventis CropScience GmbH (DE)
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YMSQWDHAYFDEDGRSAVAEDPAFAEMFTYQKKLVDDLGGFEKLEKYRNTFGDEWGAR
HPFOGTSOYAMQLDGEWRUKGMAKDGYDFEIGTYPAWPADDBAABFGGFEGSTYWGIA
POSKKONAAMELVKYMTTDTGAVVARBNA TRNVESTFPALKSPDLKTDPEFKTPLDIA
QHREENSPPASVNOATYQLTLQDLGYQYESGKVKDLKAGLEKAAAQLDRDIEQAK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most IMPORTARY. The codon initiation codon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The length in codons is given for each CDS.

The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon.

Where these have been used to deduce the initiation codon.

Where diction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="nominal overlap with S. coelicolor cosmid St8E4A"
                                                                                                                                                                                                                                                                                                                                                                (URL; http://www.sanger.ac.uk/Projects/S.coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S.coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                           Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae maltose/maltodextrin-binding protein precursor Malx, 423 aa; fasta scores: opt: 184 z-score: 217.6 E(): 0.0001; 22.9% identity in 279 aa
Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.

Cosmid 6D10 Overlaps with cosmid C61 on the AseI-C genomic
                                              CBIO 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
                                                                                                                                                                                                                                         by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence MAY NOT be the entire insert of the
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/protein_id="CAB71196.1"
/db_xref="GI:6855382"
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                                                                                                                               Colney, Norwich, Norfolk NR4 7UH, UK
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/note="SCGDIO.04, possible sugar hydrolase, len: 421 aa; similar to SW:CELF ECOLI (EMBL.X52890) Escherichia coli 6-phospho-beta-glucosidase (EC 3.2.1.86) CelF, 450 aa; fasta scores: opt: 556 z-score: 624.0 E(): 2.4e-27; 36.0% identity in 431 aa overlap and to SW:AGAL_ECOLI (EMBL.X04804) Escherichia coli alpha-galactosidase (EC 3.2.1.22) (mellbiase) MellA, 451 aa; fasta scores: opt: 300 z-score: 338.4 E(): 1.9e-11; 25.5% identity in 459 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VGĽCNVAIGLQRKFAALLGVAPADVHLDHVGLNHLTWETGVRLGGPEGEDVLPRLLAE
HGENVAADLKLPRPLLDREGVVPSYYLRYYYAHDEVVDELRRYFSRAAEVABERQLL
WYGDPALDERPALLAKRGGAYYSEAVDLAAALLGGAGSPYQVVNTYNRGTLPFLPD
DAVIEVPAAVGGKGAAPLPVAADVDPLYAGLBANTYTAYEDLALDAALRGGRDRVFRALL
AHPLVGQYAYAEQLTDRLIAHNREHLAMA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGGLARRIFTRQGHAGRVVTTSDLDAAVDGADAVLLQLRVGQAARQQDETWPLECGC
VGQETTGAGGLAKALRTVPVVLDIAERVRRANPDAWIIDFTNPVGIVTRALLQAGHRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKLTVVGGGSTYTPELIDGFARLRDTLPVEELVLVDPAADRLEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
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Minnesota, 420 Delaware Street SE # 1060, Minneapolis, MN 55455,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Xue, Y., Zhao, L., Liu, Hw. and Sherman, D. H.

A gene cluster for macrolide antibiotic biosynthesis in
streptomyces venezuelae: architecture of metabolic diversity
Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                     /product="putative sugar hydrolase"
/protein_id="CAB71199.1"
/db_xref="G1:6855385"
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/strain="ATCC15439"
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0; Mismatches
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/gene="SC6D10.05"
4000. 4017
2690. .3955
/gene="SC6D10.04"
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/transl_table=11
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/transl_table=11
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91.3%;
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(EMBL:AL122662) Streptomyces coelicolor probable sugar transport inner membrane protein SCF11.20, 299 as; fasta scores: opt: 662 z-score: 806.9 E(): 0; 38.4% identity in subtilis probable ABC transporter permease protein YeSO, 299 as subtilis probable ABC transporter permease protein YeSO, 296 as; fasta scores: opt: 588 z-score: 17.5 E(): 1.5e-32; 33.2% identity in 304 as overlap. Contains Pfam match to entry PF00528 PPD_transp.

Binding-protein-dependent transport systems inner membrane component. Contains possible hydrophobic membrane spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKYDGFGVPQFRGLENWAYVFQDYPLFWPALRNTLWLVLVMVTCRVVFGLGVGLLITK
TRGAGVFRFRLFYLPYLAPPVAATLAFVFLLNPGTGPVNSVLEGLGVPAPGMFTDSAM
SKPALFALAVWGVGDLMVIFWAALLDVPKEQYEAAELDGASAWQRFRFVTLPNISPIV
LFAVVTGVIQTWQYYTQPLVAGKVASGIIGGSGOSFEPGYPDKSTLTLPQLVYNLGFG
RFDYGSACVVALVLFALAMAFTALLMRRGGLIQAGDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1376. .1654
//gene="SC6D10.02"
//note="Pfam match to entry PF00528 BPD_transp,
Blinding-protein-dependent transport systems inner membrane component, score 59.00, E-value 1e-13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Binding-protein-dependent transport systems inner membrane component, score 64.10, E-value 3.1e-15"
                                            /note="SC6110.02, possible sugar transport system permease protein, len: 314 aa; similar to TR:09X6C4 (EMBL:AF135398) Thermus brocklanus puttative integral membrane protein BdtF, 280 aa; fasta socres: opt: 498 z-score: 582.4 E(): 5e-25; 35.4% identity in 288 aa overlap and to SWIACF AGRED (EMBL:X66596) Agrobacterium radiobacter lactose transport system permease protein LacF, 298 aa; fasta scores: opt: 437 z-score: 511.6 E(): 4.4e-21; 31.1% identity in 315 aa overlap. Contains Pfam match to entry PR06528 BPD_transp, Binding*protein-dependent transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAALFFTLPFVFVVLTSLMSDQQALTRDLWPHTWEWGNYRAVLDTPGFLTWWKNTLLY
AGLGTVLTVASSVPVAYALAKFRFRGRHLSLMLVISMMLPPQVIIIPWYLFWAKQLD
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Gapne="SC65010.02"

/note="PS00402 Binding-protein-dependent transport systems

inner membrane comp sign."
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/db_xref="GI:6855384"
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1771. 2682
/gene="SC6D10.03"
/note="SC6D10.03, possible sugar transport inner membrane
                                                                                                                                                                                                                                                                                                                                                           systems inner membrane component and match to prosite entry PS00402 Binding-protein-dependent transport systems inner membrane comp sign. Contains also possible N-terminal region signal peptide sequence and possible hydrophobic membrane spanning regions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative sugar transport system permease
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                               /gene="SC6D10.02"
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/transl_table=11
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/transl_table=11
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vocofgringhtherrerdptaclelsspolltherrerpay
vshcsovgylkhtherrergtaavasfaellebegvyvzpwwepetfadowysadyvrrd
rtvarvsksvkgonatreepthyhthyppwgrg
rtvarvsksvkgonatreepthyhthydppgkgyrhfsdyhthiltheqaeyeaaftaadglr
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VYGKVSSPLLKLTKCTHKLTISGFAMSATPLSLELGWVTPAAADATIAKAVESARKAR
TAVVFAYDDGTEGVDRPNLSLPGTQDKLISAVADANPNTIVVLNTGSSVLMPWLSKTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGLAAVPVGTDHLIHEYRVEWAGEPRPNHPAIAFDEARPEPLDWDHALGIEAILAPY
FHLLANNDSMVDDLVDFARSWQPDLVLWEPTTYAGAVAAQYTGAAHARVLWGPDVWGS
ARRKFVALRDRQPPEHREDPTAEWLTWTLDRYGASFEEELLITGQFTIDPTPPSLRLDT
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anvQytsraaelvaqmtldekisfvHwaldpdrqvipgvprlgipelraadgpng
irlvGqtatalpapvalastfddtwabsygkvwgrdgrallngpwylgpwmnirvphg
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REIEFPAFEASSKAGAASFMCAYNGLNGKPSCGNDELLNNVLRTQWGFQGWVMSDWLA
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RIVGQMEKFGLLLATPAPRPERDKAGAQAVSRKVAENGAVLLRNEGQALPLAGDAGKS
                                                                                                                                                                                                                                  ALAELTALLADSDDSPGALLSALGVTAAVQLTGNAVLALLAHPEQWRELCDRPGLAAA
AVEETLRYDPPVQLDARVVRGETELAGRRLPAGAHVVVLTAATGRDPEVFTDPERFDL
ARPDAAAHLALHPAGPYGPVASLVRLQAEVALRTLAGRFPGLRQAGDVLRPRRAÞVGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLPTVGMRYVPYNGTSVVPDMLSEPPARPRVCLTLGVSAREVLGGDGVSQGDILEALA
DLDIELVATLDASQRAEITNYENTHYRFTDFVPWHALLESCSAIIHHGGAGTYATAVIN
AVPOYMLAELWDAPVKARAVAROGAGFFLPPAELTPQAVRDAVVRILDDPSVATAAHR
LREETFGDPTPAGIVPELERLAAQHRRPPADARH"
                                                                                                                                                                   GVPVPQQVLŠYGEGCPLEREQVLPAAGDVPEGGQRAVVEGIHRETLEGLAPDPSASYA
FELLGGFVRPAVTAAAAAVLGVPADRRADFADLLERLRPLSDSLLAPQSLRTVRAADG
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                                                                                                     /translation="MTDDLTGALTQPPLGRTVRAVADRELGTHLLETRGIHWIHAANG
                                                                                                                                        DPYATVLRGQADDPYPAYERVRARGALSFSPTGSWVTADHALAASILCSTDFGVSGAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRVLLTSFAHHTHYYGLVPLAWALLAAGHEVRVASQPALTDTIT
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/protein_id="AAC68678.1"
/db_xref="G1:3789895"
   tautomerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="glycosyl transferase"
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                                  /protein_id="AAC68676.1"
/db_xref="GI:3789893"
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/product="putative
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1475. .2755
/gene="desVII"
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/gene="desVI"
2845. .3558
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/gene="desVI"
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/gene="desR"
3625. Fr
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/gene="desR"
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TITED I ALL TOOL "METALISATA PA BERCAH PGADLGAAVHAVGOTLAAGGLVPPDEA GTTARHLYNRAVRYGNSPFTPLEEARH BILGYDRDAFRELLALEGOVPELRTAVETGPA GTTARHLYNRAVRYGNSPFTPLEEARH BILGYDRDAFRELLALEGOVPELRTAVETGPA GATWANTLLPLEGGSGVPELTANFSSTOLPPSSTOLPAGNAF SOGLEPLTNPGLGSLAAHAT BHGLRPYTYNBSF ALTERTLER OP GLWGLHAIRTSLYGLNDESYEGTTGKKAAFRRYRENLRRFOLLRAF ESPINGFAYTVLPGRASRILLDLYNPETADLNDAGOGRIDFYN IREDYSGRDGCKLPO PERABLICANTAFFROLL BOYGYLALNSLRF RAPTWRPTAH PO VANOV POLLGDYLLRER GASPEDLGARNY I AGRAY TOT STATT BARBAT POLGANTAR LAND STATT BY TOT STATT 
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ALTIGONIFHCPGLYTLLRDSIARLDGCVLFCYPVKDPERYGVAEVDATGRLTDLVEK
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FAWLDTGTHDSLLRAAQYVQVLEERQGVWIAGLEEIAFRMGFIDAEACHGLGEGLSRT
EYGSYLMEIAGREGAP"
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                                                                                                                                                                                                                                                                             TGATPVPVEPHEDHPTLDPLLVEKAITPRTRALLPVHLYGHPADMDALRELADRHGLH
                                                                                                                                                                                                                                                                                                                                             IVEDAAQAHGARYRGRRIGAGSSVAAFSFYPGKNLGCFGDGGAVVTGDPELAERLRML
                                                                                                                                                                                                                                                                                                                                                                                            RNYGSRQKYSHETKGTNSRLDEMQAAVLRIRLAHLDSWNGRRSALAAEYLSGLAGLPG
IGLPVTAPDTDPVWHLFTVRTERRDELRSHLDARGIDTLTHYPVPVHLSPAYAGEAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MRLLVTGGAGFIGSHFVRQLLAGAYPDVPADEVIVLDSLTYAGN
RANLAPVDADPRLRFVHGDIRDAGLLARELRGVDAIVHFAAESHVDRSIAGASVFTFT
NVQGTQTLLQCAVDAGVGRVVHVSTDEVYGSIDSGSWTESSPLEPNSPYAASKAGSDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="TDP-glucose-4,6-dehydratase"
/protein_id="AAC68681.1"
/db_xref="GI:3789898"
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/protein_id="AAC68683.1"
/db_xref="G1:3789900"
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/product="transaminase"
/protein_id="AAC68680.1"
/db_xref="G1:3789897"
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complement(8424. .9302)
/gene="desIII"
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/product="4-dehydrase"
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ARIRALHNFGFDLPGGSPAGGTNAKMSEAAAAMGLTSLDAFPBYIDRNRRNHAAYREH
LADLPGVLVADHDRHGLNNHQYYIVEIDEATTGIHRDLVMEVLKAEGYHTRAYFSPGC
HELEPYRGQPHAPLPHTERLAARVLSLPTGTAIGDDDIRRVADLLRLCATRGRELTAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC005928 37969 bp DNA linear INV 24-FEB-2000 Leishmania major chromosome 3 clone L6290 strain Friedlin, complete
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PORYOWERRHISSSLAVSPSPSSASSASHASHIDAYEVAVABETRTDVGGSLLQQP
TSLBSCTVKSYGTA.DISDDGSRSSLSAVAVAVHTVANTFDLMTQTVGYRTPSTRAEV
OPGQLEHHAQHPQQRQGQVMSSYAVEFSAYDPHSFTLLDGNAHHVGGYGQSEPAPLAR
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Cawthra,J., Marsolini,F., Sunkin,S. and Stuart,K.D.
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VELVMRRVGSTSLLQFLWVVLLVVMLLVGNAFQVIFLNFWIHQFPTKLNPQIAPASSS
ADEHGLRLYFDAAHALGCAVDGRPAGSLGDAEVFSFHATKAVNAFEGGAVVTDDADLA
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Submitted (24-FEB-2000) Seattle Biomedical Research Institution, 4
Nickerson Street, Seattle, WA 98109-1651, USA
On Feb 24, 2000 this sequence version replaced gi:6425646.
Location/Qualifiers
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                                                                                                                                                                                                                                                          Gaps
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                                                                                                                1757 t
                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                          71.5%; Score 18.6;
84.0%; Pred. No. 7e-
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/db_xref="G1:7025826"
                                                                                          HRDTAPAPLAAPQTSTPTIGRSR'
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                                                                                                           4686 g
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/clone="L6290"
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EAHEPVASDSSDGTASGGVAITPAASPDEPATSRVNEHGAVHDLSGVEDGEYLRFTAT
GAPELETRIMETVRYNGEDTVVKLVMLAGETVIOLCFTLCLLPADALPWGNSETVS
ATLDNFAEGIRCVFTIRDHELYCFLYTLGFVFTYVGCAYLNHYSAALCSIVTOLSSPV
TALMLVIVPGWNVQVDGDSPRYYNMFAIFFLCVAALLIYVMWEEMTDAEKVQAEYELKM
KELRVRPSSHEAPHLVTWQG"
                                                                                                                                                                                                                                                                  LIAFPTLINMTDDASPWYVSVFAIFLLSCGTVLYVYNDEMTVEFKAVGEMOLKWAMMOE
QSPRHAPSLABGQRYHEVDSGVNGSSLATSQSGVSQPQQQQHRHARSRRYCRRRQSGY
AVVVDQDASDASASGQPHRY"
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VAHQPSSCPSAPASVDWQLTINSSAVLQWWQREYDPFLLGCDASAHRTAGPTPPATTA
THVLASTRYSAHVGPPAPPLGYPDYIAIEATQHTEGVLRGETYAYHHAAAVGAVPAPP
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YAASALLDRWCLFGEAAAVVPSMPASSGATLDGTQQSQRPHDAAAHHLRIAELALGAG
LLSNYRAVWLNGAVLSHPGTARSVLVVGPRRSGKTTLALHCLSAAAMQASSSASGDGG
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DMRALLEQDLNGIDYIAFCSRCAVDSLSAALDHRYGGGGESVSERAGSAPAVNEDRRA
TAVVKVLAKCALAAIGKDADYVFERLRIRTTICPDEPSPAGIAAKLAESGRAEGRTIA
                                                                                                                                                                                        HQQHIPHSEHLLHGEDASVKLVMLTSDTAIQAILAVVLMPMDALPWFGGSHSIREVVQ
NLDEGIDCVLHCPRNMRYCILYSTGFVLVYIASAYLNRYSVTLCSMVSQLSGPITALV
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LISFPSDGTPGNYTAFAVPGIFFAVLFVLLLGAYTAIRRPSLRFARHAHGWVILIGVG
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TICGILAASLYGLIKDHNMGEGKWWILIFFLSMPFRVLMNVWQSLYMIVYTHDPNFVL
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SIARYNDRTLMSGLEDEEDDKEELRNARPARHAKTKLANSVKPSSVDANDDDAVGDST
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VNTLAGVVLLDWNVEELASASPTPVRNAVREIPLHDGGVEELLKRAQDYWFHGHHLLR
TVYDAPQDAPARLADALADEWDTAQPRSLANGTAPALHCIEGSVNFDLATQLIMSLLS
                                    AGWRLLFGIGAMDALNSALAIYAAANTPEVLQALFVSLVPIYSAIFTKWLLKDPRDYA
NPYVVVSFVLIATGVALASLFNQVVTHHHTFEDRSGSGHAGVKELLVAVFSDGSSSSL
                                                                                                                  SPVALDRRLWCFIFFLSVPPTVLMNVWQTMYMIRYTSNDQLMAYLAEHADEAECGESS
                                                                                                                                                       NDVAAGAPGQSTPLLDSARDSHGDAHHCPSPAAGEAVERVPLQPSVVSVSRSLPHGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSPIHRKHMEVLGLGVKGTANDASNTQRPAGALSREEEQLPRES
SLTTGATAAAAAAASGDVRHGPLPEEDDLSNATVVLAAAAETTATRPPIFGSGLRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDALASLPLRHLLIRGSSFASPLRITSVCLEPCHTPGAEETAAATRMTAPAHDAGANV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRLTAAEHFFLAAGMPVRRMLDPASTRLTSPTIFACSLPHHITVGLGAVLGTLRPNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLAPCVEGFTEPDVVPRFVDQLKGMGMKVVRVDAYMTRPVSEEAVSAAVTALKNGSVR
GVAFTSAGELAVLLRRSPQCLMNIDVACFGPYTAGFAAKHGVKVSCVAKDFRSFDGFA
SASSGSGTDSSSGRHAEALASSYTTFVISAVLFPAFFVVLLITYALWRRPNLRFTREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 4496" 4472...6754 /gene="L6910.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 19287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      //octe="L6220.6; predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 7404"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF35927.1"
/db_xref="GI:7025828"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="AAF35928.1"
/db_xref="G1:7025829"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /prote1n_id="AAF35926.1"
/db_xref="G1:7025827"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="L6910.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="L6910.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="L6290.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19200. .20060
/gene="L6290.1"
                                                                                                                                                                                                                                                                                                                                                                                                                              /qene="L6910.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="L6910.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="L6910.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="L6290.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                     .6754
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/gene="HEL2"

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PPPPPPPPPPPALFYAQRKECVLVLDSSRVEMSEDTHVYRLMPNFHAAAAAATRGWQR

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TDVNISWQDVVGDESAIITGGALSALPDVILAEPKKAMKYPHLTHDLIDQLARAFRVE
GHVSNRPYPATLGNANELGGWIVSQPFDELNDVVDAYVERESQRNVTERERRKQLAME
AAFVTDAAQQAESMGIRGFTAGTLAVVCSDSDEDEAAAATDGAAGTSAGKVAKKVKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSGQKNKKARSREDIIREEANLRDANKTVQDWTQQVAELCKKTDQASRLTDVADSIGL
LTAAITRMTGTSFGRNFDPGEVLKDGSAVPLQLTMWRLLVDASGMREAELAFTITDDD
ADRSPAADKKRRKSAKDKRATNLYAFGLIADLVEENITNAKSGSHGSDDWGKLERLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRAGRRGLDYLGHLJFLSVSMKKITRLMTSSMFVIKGNVQVDPITQLRLLQLYDYÄRH
RDLKGABEWSRRALGMAERLYVNPLFFAGRAAMENGNMESFFVEFAQMLLGFLHREGL
HFKDRPSSLGSLLVDAMYVFRNAQVGVEGFAFISMITRKVPAKARLARRFRYLAPSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="SRHRRPSRHMEPSASATTLAAADAAPQSAAATSSPHVHRHDTTA
TSSPAPPTQPSSSLTSSGAGDKVRATAERVGGREVAPRAVASSRDGSNGARTSDRSTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEDKYSAADSTTPDTPADRDRVGASPKYSGSAFPSLPAPLQQRTPSTRTATPPPSSSA
STSVFAPVMNAERVLRARPPALWHVAYAPTHPHTAASCGKVQLLQQRVAELWIPFTLL
PPPPSISGSSTAVSGIPATSSAEESQVTQVLRLAEAGVSCERGAADSAAAPLPLEVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VHLSAMEKFFIDGDSLLMAALSSPHVDWDLMQPLHVLHNAQVLLKGLQSRGGHFHIVF
FRHTAWFWEPTPQKLFIREALRETLTAVAATNPDSRLVVDTFDSFHSEEFAAYVSKYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEFLIMSDGEQLGHETELMHLFHNHTEEELLRFEKEGGIGEEGTPASAASATPLTDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSAVSVLPPSHRPRQKACFETPEMMQLMTMGHLLERPVIPTKDYRVVFNPDGWQRELL
DIVDNRGSAVVCAPTSAGKTFISÎYCMYSALKISNTKVVVYVAPNRALINQAVADVCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VILDEIHTMESSGNGDVWERVLALLPCPFVALSATLGETQQLCGWLNRVQQRLEAQQP
EAAKRDFTVHDIPSSGSIQRWNDIKKYMYLPPPGYHPQLKKLTAKYPNRYIHDLHPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ILTLEQLQSGFPPDITLVPSEVVQLYQKMCTLFTEHVFAKWSKVAIVQAMKAQLSMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PETYFQQE IY ITQQRARQYEADVKNAFAYWVY LNKGCDADGLETLSEGEVVAFNIDMR
ELCET ILQSFSQRLREDEAQLDKYATDAALKPEGRPVDTSAAEAEATASDTATAATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IAQPRKAFFPESKEFIADNIISVLRELNSRDMGPTIVFTFEGEDCDDLTKAIIARLED
AEAAYRQTEEFAQYKATMERKAAAAEAARRQRESTLKQKKLTTDDGGEVDRADRDVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NMNDDEDYVVPDVLPEFTF1GQYCTVDP1VVKEAVEEC1KRGDTLCARA1QRGVGHH
AGVKGKLRRMME1LFRGRHCGV1CATFTLALGVHSPCRSVVLAGDHVLLNTTQFRQMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVVQEAKAELLAYLFSVNKVCGVPLELHRSALSDPAVIELWSGRRVAKQHRVVLAPLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VCSPATKPFSYVSVFRMISAFYTYLASTLKEPADTRLPYMCAKTKKKHCIFGGTSDMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHDGAQVLINACITDFVRCKAQIDSVRSNFRFTLLEELNGLSQSESYAVLNQTERLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAVPQVNDPSQPLARPQTSAFASPPPPTAATGGSRRRARMPLVFVVAPRLIASFIHHG
ALCSLELMSQDWELTPENMVLLLIALFETLNPPAGDGRVSVDDAERMEHLRETVAAMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VDGGGSSALAAAYSEEEHQLGMEYIRRAHPHLFRRYVGPLSESASAARDGMPSLPVSS
ESRGGLSASANPNIAAAAATGGGMVQRNHRDMYFDSGSAVTATGSDSVRPSASPHSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTPSLMGFGTGHGRGSSGALAPHVLRDVSHLNTAVYDALVATYAPPSEPSPVSPP
PPLCPTLGQQQPRPTAATAKPVVMLLDSPALLADAEGVRLFQSGVRGVQQAVVSTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGDAGDNVQEARVACVLRNVRVSATAARKFSSTVNPLLNASNGGSPSTTQRTSLRFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QSSTAPSPAGDVHTCHLPRGLTLHCRNMYLYGHLRVFGNLVLDSCVFVGSLTTEELAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MSSHYRELNQLFVDANGQPDFDATVEISASLPIKQLFQERSLLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PSSSNSEATAASNASPSTVKPVHETTALLRTCNAVLRWAAAEKAGQDQGGAAVAARAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVGQIDSLQSPDECRMAWKFLATFAGQPAALVCIDKALTEVAVDFHYAMARPRQFDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRENAVVVFAVTVSSGNFARSLVLEPNSTKLAAALERAVPLPTLSDASLALTKDGQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RREQVVSAAVHAYLHAGDSTPPRTEQQRQLCQVMVTTAYCTALVSAELRAQRSVTSPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VKKDFTVYDATSYLNWVYLTYVQLHFQCKLMTRVVRLQLMQWKNERERARQAQEAPNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NVGVPLFLYCHHKVLACIRDNGVAISTDDLDAVRSALAHFDFPASYYEKVDGAIAKWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYGSKKYSFPGRNVYGVHGGADYHRYVDSCQVLVTLPEVLETLLLSPKYKEWAKRLDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QQQQQQSDDDANSVPTATTPQPYNDFQCRLVALGEARRPPLTSEGHMALPENADGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLELKQRITEDQTMELKRPYRSLVDDESHGDTVAFYYHCFLTWATARRIKVAYSSRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAAFLNEMAPYLLQAFQHCDCATGRGTEFDVYDGHLITIMAHLLRTTPAEQLLDEDGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LMAKLKETAEPYAARDPFVAISGCGDHFVHSEDLVTTLRRGLFCDRRMLPVLDLTDGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NISGLTRDDKYTPLQVLSALYPERERGENVABEDLKFYAGTLGVMDFASQLHELRPHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               //orte="L6290.3R; predicted using Glimmer, Testcode and CodonUsage; Glimmer predicts start codon at 15410" complement(29757. .>37969)
/note="L6290.2; L6910.1L; predicted using Glimmer,
                                                                                                                                                                                                     /note="Blastp similarity to helicases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(29757. .>37969)
/gene="L505.2"
                                                                                                complement(22336. .28971)
                                                                                                                                                                                                                                                                                                /product="Helicase 2"
/protein_id="AAF35923.1"
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                                                  Testcode and CodonUsage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKELAMVQWMARIAEMRRARK"
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                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GI:7025824
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                                                                                                                                                                                                                                                            /codon_start-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myler, P.J., Sisk, E., Hixson, G., Kiser, P., Rickel, E., Hassebrock, M., Cawthra, J., Marsolini, F., Sunkin, S. and Stuart, K.D.
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TPEEVQRRTSEVFEWVASKQVQLTIGHEYPLHEAAQALADLQSRKTTGKLLLKCID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MEVIATAHGGPEVLAVRPSSHTPDATQLEGGQVLVHNAYAGVNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDTYFLSGLYKKPAMPY IVGEEGAGAVVKVGAGVPETMLGKRVAYFGGAGCTGSYAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (15-NOV-1999) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA (bases 1 to 41944)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-NOV-1998) Seattle Biomedical Research Institution, 4 Nickerson Street, Seattle, WA 98109-1651, USA 2 (bases 1 to 41944)
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Feb 24, 2000 this sequence version replaced gi:6425645.
Location/Qualifiers
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
71.5%; Score 18.6; DB 3; Length 37969; ilarity 84.0%; Pred. No. 6.7e+02; Conservative 0; Mismatches 4; Indels 0;
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/db_xref="GI:7025831"
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                                                                                                                                                                   Db 14231 CCCGTCTGGGGGTTCGGCCTCCGGC 14255
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/qene="L6910.1"
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                              Similarity
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        Query Match
Best Local Simi
Matches 21;
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/protein_id="AAF35930.1"

CDS

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QQTMSAYARAVWYTEEKQGFEKPVIAVSAEEGTNVPELWEAMLKMWNARLESGQIAHL.
RRAQSTKHFYNYFEMELLAKARRMTNLEMQNMAHRVWEHEMTPREAGDIMVLRTLREH
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Pred. No. 6.7e+02;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAF35935.1"
/db_xref="GI:7025837"
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/db_xref="G1:7025838"
                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF35934.1"
/db_xref="G1:7025836"
                                                                                                                                                    /note="predicted using
possible frameshift at
                                                                                                                                                                                                                                                                                                                                    /product="L6910.12"
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/qene="L6910.15"
                                                             LAADAAVQHDAGKRA"
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/gene="L6910.5"
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                                                                                                                                                                                                                                       . .17086
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                        /translation="mklikfvnsdaphtladvqlrnqrlwfpcrhgnaavaakswtlt
Aaspasvsggywlldddsqplceitdvllalpetaanaagssgtfaprgytdkdvdgi
Dfrskmgrqmereratygatsktatksartmmnaeemtekknermkrereavaeaied
                                                                                                                                                                                                  /note="L6910.2; predicted using Glimmer, Testcode and CodonUsage; ORF starts at 5110, Glimmer predicts start codon at 5110, Testcode and CodonUsage predict start codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRRLTAVHVAGRPHLCLINAALRRKAGGNINGELINGELTAVETAKGGGGGTERONGER
POYOPPHLTDRPAYRNIEDATGVQQELEDDKGCVYCVESHLSSLMTYLRDEGRRADA
TDPVDAASGGASAGGGGPESVYTMDRLRRLGAELQACPYTATRLLLAGADVAFTPY
GYVLDEGORAVLLGGAATUPATAABAAAVAPAPSRSTPAASGGGALONUVAPHSPPSL
GTVLZHRRQRYTATATFRRRRQQQQRGGNVTGGDDDDGGEEBAIWSTWARSAPPSPSL
GDIFVPDBAHNTADHCRSTSTYTVAPAPHILLLARRLFETYLARYASRLLTRNKQRLREL
VHFLSKLSGFCERADSAAVLGGGGGGGDIAPSLASAPSPPLMRLDQPSTTTPTTAART
LVLPFHFTELDAGIDSVUVYAPTTFLVDSQLLMKLQGFYSYALDABCLQORRESVSTAM
RTTMTVSGTDSSAGSTAGVKRQRGSGVGVSDAHNBAQRRILLASLDLPDNHKKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGEAAPPHLSLAEHLSQOLOPAGVAWTAAAHAGAVAPADPVOLRALTAEALQCVERLL.
CALYVSNTTSTRVLWTPSSLSPTSPARPAGCAVROGALKVIOLEPGMYTFAPLVLEAR
AVVLAGGTMQPLAFTCGPLLPAQAMVGGDAGGDCGTASTIGRSAVEVAVEGIGGSDYV
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EEENPVEHRWVPTAVAQRGYEAAFTLSITRNATVHYLTFYLDAAFTSKTNPGANFVLA
VRPGGENNWTEVSVGLREPLPVNVGEKIQGTLRIYTPADKGGKITVVEVTAKTEGQVA
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SNAASTSNDTGSSRIGVSSIISPHAHRVLAEVGCTLLNLARVLPPAGAICFFTSYDVM
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TITHGSILGDKTRMEKLGTHLNSYIRPSPSGGHLGGVTSRAWEALEIFERARFDVVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HDSEKAALDYSPPSPTLDEVLRQRQLEEEMVQVRRERRARYRAQRRQIRQARKLMRLO
QQLTNSGGEHDFLLTQDPLAWYAEQLSMKKARLRGDDLVDLHSASSLSSSSSSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SAREDDDDAEAQLEAALSTLIPLRKPKVYFASRTHTQLQQLMEDLQRTAFARLPLRPR
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GSASTPSPASSSPFTCAEEWGLYMDSMMRTVNQCIGRCIRHAGDYATIILLDARYTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MLLNSILSYLFDPVEDAKDVDGTASGSGSSVVAEPPAAMATAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HRKIEPLESAAGRTAGEGMGGVNDTDDPATSSKSLGSPTHACPVAAASRPTPSRQQQQ
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12821. .13870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="L6910.10; predicted using Glimmer, Testcode and CodonUsage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="Protein Arginine MethylTransferase"
                                                                                                                                                                                                                                                                                                                                                                                        /note="Blastp similarity to CHL1 helicase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PDARRRVSAWLQPSMRVAQTFGQCFSGVREFFAERQPKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Helicase 1"
/protein_id="AAF35931.1"
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/db_xref="G1:7025834"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:7025833"
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db_xref="GI:7025832"
                                                                                                                  NDASVMEPRKKERKHSKK"
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/gene="L6910.11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10078. .11295
/gene="PAMT"
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                                                                                                                                                                                                                                                                                                                           5389. .9468
/gene="HEL1"
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                                                                                                                                              5389. .9468
/gene="HEL1
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AATLLEMTLQTHGLLCGGGVPSQAWSPTPDPADASSGGSSTAALNGTVLLDKFPRLSA
EMLLQHVTYLLSNEAKQRTANAADGAGEGSDS1YLSPQRTRHFGLTGVETLLLSATQA
EQVNQVLPLYVRGHTLPDEVASDITQTRNIHBAVRKTQRVLSRVLQQASQELASQSGS
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TGIDLVKLSASIQAATWQAIQKVRAAKEETHSRSLRRNPQVLAEARLRDWYEQDANTL
                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MLEHRRLFPGRRYDSRVYRSCASPMPYLLEEKLRGTAMEQRTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEAVISCPATPGLAEGKISAYLLDLATRTLRPPTFPPLSDSTVTAKDTVCLVGGPELA
WLAVGMTPFRNITSVTLQQGELKSCSLQESMEWMRLAHLLKAAPEQVNGDGGEALALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRLAAVRTDLVLLDLLANGHPTTGLPQVLATPFADVLDAYVDMEKEQHSAAAPSAPQN
VGRLRSVLFDEEPVTGVHLEQPSLRLRLVSLQQLLVRIVRALSGAHVGLPAGNRPTPH
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VLRDEDCDPANIPIGSVHPLFAPGLLOLEVDPNVATNGGSRVDEFFVLSEQRKEMRRD
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AAPATSGGAGSSQASSTTTTASSSSSSNSNVTSSSSSAGSTPKGAFNPAEWKMAVGD
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LLHAQRCIEEAAHYVDALTKRTNLLLDGLKERTHEPELGLYMLLQAEIAARVFDWDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTAAVDDAGHNGPHPALAHLPSHLFVRTAGARGPPPGWEYYGVHLGIKAEAMNVRYNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSFRYTNHLVATLKHRLFLEAAHRQLVRQTFTGVCNGIEVTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVVEAQKDNAKSLLLLERGIDILNSVGGVRNPTVANLLRPLYAARFEMLNGSEHLPRS
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GEALDRALKLNRMLYPDFRQNAPAAATLMTMACMYADTRDYLYATGLFESANKAVTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPELIDAVGLMTRHSRSSRAESTASASTSAAESAMSRALPPTRWTTTVSATAQPTTDA
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Glimmer, Testcode and CodonUsage;
5' end may extend start codon to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17277. .17807
/note="predicted by Testcode and CodonUsage, but no ATG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="predicted using Glimmer, Testcode and CodonUsage;
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18721. .19698
/gene="L6910.14"
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/translation="MKLVPVALLYLGSLAFLGADFARLDVASEFRKWNKWAVSRGKR
ELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQTSGPDAARIRVKRYRQSMNNF
QGPRSFGCRFGTCTVQKLAHQIYQFTDNDKDGVAPRSKISPQGYGRRRRRSLPBFGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces fradiae NDP-hexose 2,3-enoyl reductase TylCII (tylCII), NDP-hexose 4-ketoreductase TylCII (tylCII), NDP-hexose 4-ketoreductase TylCII (tylCII), NDP-hexose TylCIII (tylCIII), mycarosyl transferase TylCV (tylCVI), and NDP-hexose 3,5- (or5-) epimerase TylCVII genes, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The mycarose-biosynthetic genes of Streptomyces fradiae, producer
                                                                                                                                                                      Submitted (02-FEB-1998) Molecular Cytogenetics, Mayo Clinic and Foundation, 200 First Street, SW, Rochester, MN 55905, USA 4 (bases 1 to 1466)
                                                                                                                                                                                                                                                                                            Submitted (19-JAN-1999) Molecular Cytogenetics, Mayo Clinic and Foundation, 200 First Street, SW, Rochester, MN 55905, USA
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Submitted (30-APR-1999) Biochemistry, University Of Leicester,
                                                                                                                                                                                                                                                                                                                                           Sequence update by submitter
On Jan 20, 1999 this sequence version replaced gi:3372495.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.0%; Score 18.2; DB 4; Length 1466; 87.0%; Pred. No. 1.1e+03; Live 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 5908)
Bate, N., Butler, A.R., Smith, I.P. and Cundliffe, E.
                                       Imoto,I. and Jougasaki,M.
Cloning of cDNA encoding canine adrenomedullin
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="adrenomedullin precursor"
/protein_id="AAD05423.1"
/db_xref="GI:4164450"
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Location/Qualifiers
1. .5908
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                                                                                                                                                                                                                                                 and Jougasaki, M.
                                                                                                                                     Imoto, I. and Jougasaki, M.
Direct Submission
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Matches 20; Conservative
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ELRVSSSYPTGLAEVKAGPAQTLIRTQDVKGASRNPQTSGPDAARIRVKRYRQSMNNF
QGPRSFGCRFGTCTVQKLAHQIYQFTDKDKDGVAPRSKISPQGYGRRRRRSLPEPGLR
                                                                                                                                          MAM 28-JAN-1999
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 1432)
Ono,Y., Kojima,M., Okada,K. and Kangawa,K.
CDNA cloning of canine adrenomedullin and its gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="encodes proadrenomedullin N-terminal 20 peptide"
                                                                                                                                        CFU96127 1432 bp mRNA linear MAM 28-JAN Canis familiaris adrenomedullin precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-APR-1997) Biochemistry, National Cardiovascular
Center, Fujishirodai 5-7-1, Suita, Osaka 565, Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Butheria; Carnivora; Fissipedia; Canidae;
1 (bases 1 to 1466)
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                                                                                                                                                                                                                                                                                                                                                                                                          the heart and blood vessels in endotoxin shock
Shock 10 (4), 243-247 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="adrenomedullin precursor"
/protein_id="AAD09957.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ono, Y., Kojima, M., Okada, K. and Kangawa, K. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Canis familiaris"
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426 c 401 g 299
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                         Db 38425 CCCGTCTGGGGGTTCGGCCTCCGGC 38449
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                                                                                                                                                                                                            U96127.1 GI:4193235
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       adrenomedullin
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Best Local Similarity
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                                                                                                                                                                                         ACCESSION
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ELVDGSPDDLVLDIGSNDATLLKAYPECPRIVENTER
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VILQYCGIGERDLPCIGEVSPEKAGRFTPGTGIPIVSEEDAKAMRPDQLLVLPWIYRE
GFVERERDFLAGGGRLVFPLPRLDVV"
                                                                                                                                                                                                                                                                                                                                                    /translation="MSGMYVQLGRGATLVSRLWLGTVNFSGRVPDDQAIRLMDEALDR
GVCVDTADJTGWRLXYGHTEELVGRRAKGSGGRDDVVLATRYGEPWASDRVNDRGLSA
RHVIRSCEASLRRLGYDHIDLYQMHRWDRTVRWDELWQAMDQLVASGKVRYIGSSNFA
GWHLAAGQESAARRGSLGLVSEQCLYNLAVRHAELEVLDAARRYGIGYPAWSPLHGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSGALRKLAEGTAVKSGQGRAQRTLPALRDTTARYERFCARVGRDPAEVGLAWLLSRP
GVSGAVIGPRTTGHLVSALRAVELELSEEEHRELEALFPPVGSGGEVPEAWQN"
complement(1066. .2109)
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RDLLDVRDAATAFTTALEHADOLRGKHWVVGTGRRHRLDRVFGTVAALAAEHTGRPPV
PVVTVDPPGYAEVCDFRTPDSDPSAFRAVTGWRPRAEPADGIAAAIAAVAGAGDSPEP
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SEHINVGLMRELAEALRPTGPADATRAPVVLFGSTLQAGMEQAHTPGTYAAQKLAAER
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AYDIVCHEHLEYYALQOIEWMAERAGLIVLRAELTDVYGGSLCVTLARASSPHPRDEA
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                                                                                                                                                          'function-"biosynthesis of NDP-mycarose during tylosin
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/function="biosynthesis of NDP-mycarose during tylosin
                                                                                                                                                                                                              /codon_start=1
/transl_table=11
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                         complement(80. .1069)
/qene="tylCII"
                                                                                                       complement(80. .1069)
/gene="tylCII"
/db_xref="taxon:1906"
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/note="orf8*"
                                                                          /note="orf10*"
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/gene="tylcv"
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3575. .4960
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/gene="tylcv"
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bldA regulation; cytochrome P450; hydrolase; integral membrane protein; LacI-family transcriptional regulatory protein; protein; LacI-family transcriptional regulatory protein; prolyi aminopeptidase; RNA polymerase sigma factor; ROK (NagC/XyLR) family transcriptional regulator; secreted solute-binding lipoprotein; TetR-family transcriptional regulatory protein; TTA codon.

ISM Streptomyces coelicolor A3(2)

Streptomyces coelicolor A3(2)

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomyclneae; Streptomycetaceae; Streptomyces.

Is (bases 1 to 22396)

Redenbach,M., Kieser,H.M., Denapaite,D., Eichner,A., Cullum,J., Kinashi,H. and Hopwood,D.A.

A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome

Nol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MITTETRVRDAYRITPEPIPDHRGSLYESLRYETLRRATGHAIE
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EPPYRSERDAAAPSLAEAAAGTLPGYEQCLRAYPAM"
                                                                            IELTARAEKLLKEHGTTSDPVAFAATVQSGPGLFYMPRYFQYAGETFDDRHHFVGPCA
PRASHGHGWAQREDGRPLVMVSLGTITNBRPGTFRAÖVERSFRRRWILLVLGGGLGA
GDLGPLPENVLYNDFYPLGDVLHTDLLVHHGGTSTAARALAHGVPTVAMPERBEPA
TARRIAELDLGDWLLPGEVTAEKLSGIAQRVLTDDRIRKGLDRMRGEIRRAGGPAVAA
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                          RVGARAVTYPLDRERFRADMVPKEESDEYTDEGEFLKVLEWLLDTTADTLPLLESAFA
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GRFRRAPDEGSCRMAHIAFFILPAAGHVNPTLGVAEELAARGHRVTYALPEDMADRAV
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/protein_id="AaD41825.1"
/db_xref="G1:5305795"
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Thomson, N.R., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.0%; Score 18.2; DB 1; Length 5908; 87.0%; Pred. No. 1.1e+03; Live 0; Mismatches 3; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2078 g
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                                                                                                                                                                                           /gene="tylcvii"
/note="orf6*"
5004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4514 GTCGAGGCGTTCCGTGACCGGCC 4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
                                                                                                                                                                                                                                                                                                       5004. .5597
/gene="tylCVII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 gictaggcgitcggigtccggcc 26
                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         853
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SCF43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
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JOURNAL
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VERSION
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REFERENCE
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Streptomyces coelicolor sequencing at The Sanger Centre is funded

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protein, Orf3 (339 aa), fasta scores opt: 2115 2-score: 2334.5 E():0 99.4% identity in 329 aa overlap. Also weakly similar to Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphatase (231 aa), fasta scores opt: 186 z-score: 245.7 E(): 2.6e-06 41.9% identity in 86 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="IDADDAIEATASADDVDAGKPAPEPVEHALELAGVPAERAVFVG
DTVWDMRAGSRAGVRCYGVLCGGLPRADLEEAGAEAVYADPADLLASLRGSPLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="SCF43.02"
/note="SCF43.02"
/note="SCF43.02. possible integral membrane protein, len:
379 aa. Almost identical to Streptomyces lividans
TR:P72466(EMBL:Z70724) substrate hyphae associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="SCF43.01"
/note="SCF43.01, possible hydrolase, partial CDS, len: > 98 aa. Identical over the available sequence to Streptomyces lividans TR:P72465(EMBL:270724) substrate hyphae associated protein, Orf2 (218 aa), fasta scores opt: 648 z-score: 826.2 E(): 0 100.08 identity in 98 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.nih.go.jp/
jun/cqi-bin/frameplot.pl. CAUTION: We may not have predicted the
                                                                                                                    (URL, http://www.sanger.ac.uk/Projects/S_coelicolor/)
CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct initiation codon. Where possible we choose an initiation
                                                                                                                                                                                                                                                                                     The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS. Usually the highest scoring match found by fasta -o is given for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions.
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by the BBSRC and Beowulf Genomics
Details of S. coelicolor sequencing at the Sanger Centre are
available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence MAY NOT be the entire insert of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:100226"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   upstream initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "SCF43.01"
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xylose repressor (399 aa), fasta scores opt: 519
z-score: 575.9 E(): 1.0-24 28.18 identity in 402 aa
overlap. Also highly similar to Streptomyces coelicolor
TR:087855(EMBL:AL031013) putative transcriptional
regulator SC8A6.21c (441 aa), fasta scores opt: 2034
z-score: 241.7 E():0 71.48 identity in 434 aa overlap.
Contains a pfam match to entry PF004480 ROK, ROK family and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EAVAAAGVPALVIASSYGAYSPEPKNHAVDESWPTHGWPDAAYCREKAYLERÄLDTFE
RDHPGIRVVRMRPAFLFKRESASEQRRIFGGRFLPGPAARPELLPFLPDVPGLRVQAL
HTDDAARAYRLAVRSADARGAFNLAAEPPVDAELLGELLGVRPVRLPRAAARSAIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SCF43.03, unknown, len: 343 aa. Almost identical to
Streptomyces lividans TR:P72467(EMBE:270724) substrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MSSATGSKIVVTGATGNVGTSVVRLLSEDPEVGTVLGLARRIPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mSDHRHEGPGENGAPVPRDMPDQQAGDHDDPWEAASPTREQSEH
RQGPDGERPVDDAESAGDAETGPVPDVPDTDEAGTGRQGAPHSAAVHPEHPVPDESSG
                                                                                                                                                                                                             /translation="MWWEACAVGRAVRAAWRGPGRERDLVVQSLKAAGAALIAWTVAG
                                                                                                                                                                                                                                                 VWLGDPMALMAPWVALVLVQATVYSSVRQAGQQFAAICTGALLASAAQAIMDDNTGAL
                                                                                                                                                                                                                                                                                          VLSLPVLMLVANWSRFGGQGIYAATTAVFVLASGTAVSAAAVGHRMGQAALGAVIGVA
                                                                                                                                                                                                                                                                                                                       VNALVLPPIHLRDVRENLAALAREAGDLLHSVAADLRETQWDAQSAAGWTSDAARLER
RLEALYSARSWSRESLRLTSGRLRRLHRAPTVVPPEDEDRRWSRVTGNLGALTRTLAV
                                                                                                                                                                                                                                                                                                                                                                                             AADEHRTPAPPEGPVLDLYARLIRLIGDACHTEAGRWAGERPGADPATATEETMEELH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WSPAKTEWAAVDLASEQSDLTSHFADADAVVHLAWAFQPTHDPATTWRTNVLGSIRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WGMRLLPASPHLFDAVLRLPVMDCTRARVELGWGATRTATEVLEEFLRGLRQGAGADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative ROK (NagC/XyLR) family transcriptional
Contains possible membrane spanning hydrophobic domains."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hyphae associated protein, Orf4 (343 aa), fasta scores opt: 2274 z-score: 2584.7 E():0 99.1% identity in 343 aa overlap. Also weakly similar to Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TR:09WX08(EMBL:AL079345) putative epimerase (353 aa), fasta scores opt: 275 z-score: 318.0 E(): 2.5e-10 25.9% identity in 340 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcriptional regulator, len: 429 aa. Similar to
Anaerocellum thermophilum SW:XXLR_ANATH(EMBL:269782)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a putative helix-turn-helix motif situated between residues 30. .51 (+3.09 SD)."
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/gene="SCF43.05c"
complement(3320. .4609)
/gene="SCF43.05c"
/note="SCF43.05c"
/note="SCF43.05c, possible ROK (NagC/XyLR) family
                                                                                                          /product="putative integral membrane protein."
/protein_id="CAB66191.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                 RRLQEGLREHAGQGAARTAVLGTLLLQAENLWAEIVPEPRESAEQ"
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/protein_id="CAB66193.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein SCF43.03."
/protein_id="CAB66192.1"
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/gene="SCF43.04c"
/note="SCF43.04c, unknown, len: 102 aa."
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/db_xref="GI:6714729"
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                                                                            /transl_table=11
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                                           /codon_start=1
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SYSNVVADLVADGLVEEAGSVDSDGGRPRTLLRVAPASGHMIGVDVGETRVRVELFDL
THELBARBERLARORHDVVIVGHVRSGIRELTAAGLPPERLLGGGIGVPGTYBHT
ADRGAVVHGOTIGHMAVPLEALLRAGSPLPDTVPCI.IDNGARTLGGAEMWFGAGRGAR
NAVVLLFGSGVGASLVTPEAEQGRAVEWGHLTVRVRGRRCRCGALGCLEAYAGRSLL
NAVVLLFGSGVGASLATAALAAAAYAPADGAAADPVALATLETABYLGGAGLSDI.
NLEOPERILIGGWAGLQGARRIAAAYAAYAADPADGAADPVALAVLEETABYLGAGLSDI.
ALLPLADFFARGGRRPEPAPREHAVSYALRHBARKYTVDLGRLGPDAVTVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="SCF43.06, unknown, len: 164 aa. Highly similar to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG 06-NOV-2001
translation="MAGRNGRTVRDLRRANRTAVLQRLYFDGPLSRFELGPATGLSSG"
                                                                                                                                                                                                                                                 /psec ** Pfam match to entry PF00480 ROK, ROK family, score 22.80, E-value 1e-05" complement(4614. .4618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein of unknown function from Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
Direct Submission
Submitted (06-NOV-2001) Genome Center, University of Washington,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens chromosome 1 clone RP11-480112, WORKING DRAFT SEQUENCE, 6 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid; 32% of reads
Sequencing vector: plasmid; L08752; 68% of reads
Chemistry: Dye-terminator E1; 89% of reads
Chemistry: Dye-terminator B10 Dye; 11% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 170284 bases at least Q40
Consensus quality: 172588 bases at least Q30
Consensus quality: wum-of-contigs
Lisert size: 172934; sum-of-contigs
Quality coverage: 8.7x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
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On Nov 6, 2001 this sequence version replaced gi:13157584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.0%; Score 18.2; DB 1; Length 22396; 87.0%; Pred. No. 1e+03; 1ive 0; Mismatches 3; Indels 0;
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Direct Submission
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Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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Center clone name: RP11-480112 (sc0719)
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                                                                                                                                                                                                         complement(3785. .4033)
/gene="SCF43.05c"
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                                                                                                                                                                                                                                                                                                                                                                                 /gene="SCF43.06"
4799. .5293
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/gene="SCF43.06"
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AC098934/c
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Submitted (15-FEB-1996) W. Piepersberg, Bergische Univ.
Gesamthochschule, Wuppertal, Institut fuer Chemische Mikrobiologie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang,H.Z. and Piepersberg,W. Cloning and characterization of the mel-operon from S.lincolnensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. 1 (bases 1 to 3149)
Zhang, H.Z. and Piepersberg, W.
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mel-operon; melC1 gene; melC2 gene; ORF3; RNase H; rnhH gene;
tyrosinase; tyrosinase co-factor.
NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                  9114: contig of 9114 bp in length 9214: gap of unknown length 127205: contig of 17991 bp in length 27305: gap of unknown length 47551: contig of 20346 bp in length 47751: gap of unknown length 74121: contig of 26370 bp in length 74221: gap of unknown length 11238: gap of unknown length 11238: gap of unknown length 112188: gap of unknown length 173434: contig of 61296 bp in length.
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X95703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP11-480112"
/clone_lib="RPCI human BAC library 11"
1. .9114
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Pred. No. 9.4e+02;
0; Mismatches 3;
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/note=assembly_name:Contigl13"
27306. 47651
/note="assembly_name:Contigl14"
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"foote="assembly_name:Contig117"
ture 112139. .173434
/note="assembly_name:Contig118"
47569 a 39082 c 38186 g 48026 t ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_name:Contig112"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Streptomyces lincolnensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /chromosome="1"
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87.0%;
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Best Local Similarity 87.0°
Matches 20; Conservative
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CDS

FEATURES

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Streptomyces venezuelae putative acetyl-CoA acetyltransferase and cystathionine beta-synthase (CbsSV) genes, complete cds.
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ALEVARELGPDDVYVVLLPDSGRGYMSKIFSDEWMAGHGFLEDTSSATVADVLRHKEG
GTMPSLVHMHPDETVGQAIEVLREYGVSQMPIVKPGAGHPDVMAAEVVGSVVERDVLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MPEAVIVSTARSPIGRAFKGSLKDLRPDDLTATIVQAALAKVPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDPRDIDDLMLGCGLPGGEQGNNLGRIVAVQMGMDHLPGCTIHRYCSSSLQTSRMALH
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TLPDGTVVSTDDGPRAGVTLEGVSGLKPVFRPDGLVTAGNCCPLNHGAAALVIMSDTK
ARELGLTPLARIVSTGVSGLSPEIMGLGPVEASKQALQRAGLTIGDIDLAEINEAFAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAG48621.1"
/db_xref="GI:12082815"
/translation="MQFHDSMISLVGNTPLVKLNNVTAGIQATVLAKVEYFNPGGSVK
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TGPELWEQTDGKITHFVAGVGTGGTISGTGNYLKEASGGSVKIIGADPEGSVYSGGSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cystathionine beta-synthase in Streptomyces venezuelae ISP5230: an alternative pathway of cysteine biosynthesis Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-NOV-2000) Biology, Dalhousie University, Halifax, NS
                                                                                                                                                                                                                                                    Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="catalyses the formation of cystathionine from
                                                                                                                                                                                                                                                                                                                                                venezuelae ISP5230: cloning, sequencing, functional analysis and relevance to chloramphenicol biosynthesis
Thesis (1999) Dalhousie University, Biology, Halifax, NS, Canada
                                                                                                                                                                                                                                                                                                                            Genes for cysteine biosynthesis and metabolism in Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="putative acetyl-CoA acetyltransferase"
/protein_id="AAG48622.1"
/db_xref="GI:12082816"
                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 18; DB 1; Length 6927; Pred. No. 1.3e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"cystathionine beta-synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homocysteine and serine"
/note="pyridoxal dependent enzyme."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 6927)
Chang, Z. and Vining, L.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang, Z. and Vining, L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGQGMAMVIERLS"
                                                                                                                                                                              Streptomyces venezuelae.
                                                                                                                                                                                                        Streptomyces venezuelae
                                                                                                                           AF319543.1 GI:12082814
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/qene="CbsSV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4460. .5851
/gene="CbsSV"
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80.8%;
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                                                   DEFINITION
                                                                                                                                                                                                      ORGANISM
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     AF319543
                                                                                                                                                     KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:1200141"
/db_xref="SW1SS-PROT:P55049"
/db_xref="SW1SS-PROT:P55049"
/translation="MSYVPESIEVGYPVHTAYNQWTQFETFPQFMSGVERIEQRTDTL
THWWTSVNGYTHEPAETTEQIPDERYAWTTVGGRAEQAGVYTFHKLDDDHTKVMLQM
DFHPDSVTEKVGDKLGFVKRQTKGDLERFKKFIEERGQETGGWRGAVI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPTYDMAPWNSASDGFRNHLEGWRGYNLHNRYHYWYGGQMATGYSPNDPYFWLHHAYI
DKLWAQWQRRHRTPAYYPPAGTPDVYDLDETMKPWHDSSPADLLDHTGHYTFDTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MTVRKNQATLTADEKRRFVTAVLSSSAARYDTFVTTHNEFIVAD
TDNGERTGHRSPSFLPWHRRFLLEFERALQSVDASVALPYWDWSTDRSARSSLWAPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGGTGRSRNGRVTDGPFRAATGVWPITVRLDGRTYLRRALGGAGRELPTRAEVDSVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MRERVVAACDGASKGNPGPAGWAWVVADDTETPTRWEAGALGKA
TNNVAELTALERLLAATDRDVPLEIRMDSQYAMKAVTTWLPGWKRNGWKTAAGKPVAN
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                                                                                                                                                                                                                                                                                                     /product="Tyrosinase co-factor (MelC2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GSWISVVSHYDPVPTPRAARAAVDELQGAKLVPFPAN"
                                                                        /organism="Streptomyces lincolnensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:P55023"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           458 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative RNaseH"
Gaussstr. 20, 42097 Wuppertal, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Tyrosinase"
/protein_id="CAA65000.1"
/db_xref="G1:1200140"
                                                                                                                                                                                                                                                                                                                       /protein_id="CAA64999.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="CAA65001.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAA65002.1"
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                                                                                                                        /db_xref="taxon:1915"
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                            Location/Qualifiers
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                                                                                                 /strain="78-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="melC2"
465. .1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="ORF3"
1369, 1821
                                                                                                                                                                         /gene="melCl"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="melC2"
                                                                                                                                                                                                                          /gene="melC1"
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CDS

ORIGIN

Matches

DEFINITION

ACCESSION

RESULT 1/ AC109873

ORGANISM

KEYWORDS

SOURCE

VERSION

REFERENCE AUTHORS

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* NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 12 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                 Quality coverage: 0x in Q20 bases; agarose fp estimation Quality coverage: 0.1x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INV 20-MAR-2001
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                                                                                                           Sequencing vector: Plasmid: M7789
Sequencing vector: Plasmid: M7789
Chemistry: Dye-terminator Big Dye: 98% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 22789 bases at least 040
Consensus quality: 2572b bases at least 030
Consensus quality: 27555 bases at least 020
Estimated insert size: 16593; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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AL049768
AL049768.2 GI:6855406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1524: contig of 1524 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of unknown length contig of 1786 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4616: gap of unknown length
6190: contig of 1574 bp in length
6290: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown length contig of 1431 bp in length.
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gap of unknown length
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                                                                                              clone name: CH230-303015
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gap of unknown
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               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10116"
/clone="CH230-303015"
4570 c 4492 q 53
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                                                                   Center project name: GQIO
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VERSION
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20633 bp DNA linear HTG 08-FEB-2002
***, SEQUENCING IN PROGRESS
***, Il unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
               Gaps
          ö
       5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Baylor College of Medicine
  0; Mismatches
                                               AC109873.1 GI:18640591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 20633)
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21; Conservative
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                           Norway rat
                                                                                                                                                                                                                                                                                               AC109873
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Direct

JOURNAL

TITLE

REFERENCE

AUTHORS JOURNAL

COMMENT

/db_xref="taxon:5664"

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sequenced clone. It may be shorter because we only sequence overlapping settions once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid L6586 is not overlapped by any clones sequenced to date. It contains the left end of PAC P460 (AL160762), and the right end of PAC P986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Where possible we choose an initiation codon (atg) which is preceded by a stretch of pyrimidines or part of a Kozak sequence. If this cannot be identified we choose the most upstream initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the Hexamer program which was written by Richard Durbin as an integral part of the ACEDB-based analysis tools for the C.elegans Genome Sequencing Project. The program calculates the log-likelihood score for a given DNA segment based on the frequency of 6-mers, normalised for the base-pair composition of the genome. The program was trained using a fasta file of confirmed Leismania major coding sequences (CDS), i.e. from ATG start codon to the stop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS are numbered using the following system eg L6586.01. L6586 (cosmid name), .01 (first CDS)

To make the cosmid library Leishmania major Friedlin DNA was partially digested with Sau3Ar prior to cloning into BamHI site of the cosmid shuttle vector CLHYG (Ryan et al. 1993 Gene 131:145-150). The sequence of the packaged vector was determined by Peter Myler and Ken Stuart at Seattle Biomedical Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAR-2001) European Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, (E-mail: barrell@sanger.ac.uk) and Max Planck Institut fuer Molekulare Genetik, Ihnestr. 73, D-14195 Berlin, Germany on Feb 2, 2000 this sequence version replaced gi:4760361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Details of leishmania sequencing at the Sanger Centre are available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in codons is given for each CDS.
Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database.
Gene prediction is done using:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 40064)
Klages,S., Borzym,K., Reinhardt,R., Beck,A., Ivens,A.C., Quail,M.,
Rajandream,M.A. and Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Institute, and is available as accession number U59231. The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAUTION: We may not have predicted the correct initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon. Transmembrane domains were predicted as implemented at the TMHMM server: http://www.cbs.dtu.dk/services/TMHMM-1.0/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     jun/cgi-bin/frameplot.pl. (2) codon preference based on the codon preference based on the codon preference based so the codon preference based on the codon usage table for Leishmania at
                                                                                                                                                                                                                                        Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                               A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998)
transmembrane protein; ubiquitin activating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    on the World Wide Web.
see http://www.sanger.ac.uk/Projects/L_major/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the FramePlot program of Bibb et al., Gene 30:157-166(1984) as implemented at http://www.nih.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.kazusa.or.jp/codon/
                                                                                                                                                                                                         (bases 1 to 40064)
                                           Leishmania major.
Leishmania major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                      Leishmania.
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                                                                                       ORGANISM
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                                                                                                                                                                                                                      REFERENCE
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/organism="Leishmania major"

/strain="Friedlin"

Location/Qualifiers

(AL390693

source

FEATURES

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/note="poly-pyrimidine tract"
complement(1314. .1707)
/note="region of BLASTN similarity to: AF139112 Leishmania
peruviana clone AC16 microsatellite sequence., bases
11. .394, 83% identity over 393 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="region of BLASTN similarity to: AL483866 TA292D02P
Trypanosoma brucei TREU927 sheared genomic DNA Trypanosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGRDEEVDEELĞYKEAPKTKEVKSRQELQRERKMAKWDKKDSADKVRSKQTLRASRI
VQRNRAQWARDARNGVFDENALDAEETEALAAASRAAKQHKKLARKEALEIANDIRGQ
LRQDVDYDLEVPPAQRRRFEKSYHGSDTAGRGTEGRGSSGPEAEARTNAALKRFLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="pfam match to entry PF00400 WD40, WD domain, G-beta repeat, score 25.60, E-value 0.0012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Pfam match to entry PF00400 WD40, WD domain, G-beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:Q9NP84"
/translation="MPPTTSLTSRSSPPVATAAPRPVGAQRKPSKEVQELIDKRTEEL
KQETGQHEKKFIQGRWVTDTAALRNRGTRRREELNRRAPKRLAKYDMYYQMEEDNTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLDDHEVADRI SQRDIASGVDLQTQQRRYSLVLDKLGPYKIDFSINGTHLLLAGLRGH
MANIRWGRQLLGGETQLKDRISDRIEDLDHSWAYAQAKRYWTYKRGTEBHLLLSKWA
HMDRLGYLPKHMLLAATSSTYSTMQYLLDISTGQEVGTKVBAVMRDPTSCLAVNFSNGY
AATODLRGVYKRWSTVVPDPLLQLKGHKGVIEDICFHPNGRFFLTLGGDHAMKVWDCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLRTLEEYAVTYSFHTLDISSSGLVALGGGTNVHIWKDMFTAAKPSSPYMKFGLGYGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I A E Q V R F C P F E D V I G I G H S R G F T S L I I P G S G E A N P D F Y Y A N P H E T E R H R K E R V V T N L L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKLPPDTISMDIQVPGVNEKRLAEYNENLRLNRKARAIREKKMRRASKSLGEAAPTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYTIP (LYTI) gene; contains two pram matches to entry PF001400 WD40, WD domain, G-beta repeat; reasonable similarity to Q9557, conserved hypothetical protein (554 ag, Neurospora crassa, EMBL: AL355932, CAB91444); Fasta scores: E():0, 34.9% identity in 502 aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="region of BLASTN similarity to: AF253317
Trypanosoma cruzi LYTIp (LYT1) gene, LYT1-a allele,
complete cds., bases 4974. .5751, 71% identity over 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trypanosoma cruzi LYT1p (LYT1) gene, LYT1-a allele, complete cds., bases 4054. 4922, 66% identity over 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           590-610; good similarity to AF253317 Trypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="L6586.01, len = 679 aa, conserved hypothetical
protein; predicted pI = 9.8667; predicted colled-coil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="region of BLASTN similarity to: AQ644878
RPC193-DpnI-25G1.TV RPC193-DpnII Trypanosoma brucei
genomic clone RPC193-DpnII-25G1, bases 1. .608, 678
identity over 607 bases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="conserved WD40 repeat domain protein"
/protein_id="CAB71230.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="region of BLASTN similarity to: AF253317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat, score 7.00, E-value 66"
                                                                                                                                                 /note="poly-pyrimidine tract"
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                       /clone="cosmid L6586"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GI:6855407"
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                                                                               /note="(gcgtgt)3"
488. .512
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/gene="L6586.01"
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// viote-_royr_injuring tract.

// sole .. 6414
// note-="region of BLASTN similarity to: AQ847049
// note-="region of BLASTN similarity to: AQ847049
// note-="region of BLASTN similarity to: AQ847049
// note-="region of BLASTN similarity to: AQ84704_lm37e03 3', bases 1.507, 1008 identity over 506 bases"
// note-="hexamer gene prediction, score 72.0664; previously part of L6586.02"
// note-="region of BLASTN similarity to: AQ850952
// note-="(gct)4"
// note-="(gct)4"
// note-="(gct)4"
// note-="poly-pyrimidine tract"
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brucei genomic clone 292d02 forward, bases 1. .434, 67% identity over 433 bases"
1522. .3542
Note="poly-pyrimidine tract"
1706e="fcto)5"
Note="fcto)5"
1706e="fcto)5"
1706e="fcto)5"
1706e="poly-pyrimidine tract"
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80.8%; Pred. No. 1.2e+03;
Live 0; Mismatches 5; Indels
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Matches 21; Conservative
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Search completed: July 31, 2002, 14:01:53 Job time: 17555 sec

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July 31, 2002, 12:20:35; Search time 165.21 Seconds (without alignments) 107.049 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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72
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Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		Sequence 79, Appl		56,		5, A	1,	1, A		80,	80,	80,			Sequence 22, Appl		Sequence 61, Appl	5, 7	Sequence 7, Appli	Sequence 3, Appli	Sequence 5, Appli	251,	Sequence 99, Appl	134	4	134	134,
SUMMARIES	DI .	US-08-883-795A-37	US-08-781-891-79	PCT-US95-06815-1	US-08-706-037-26	US-09-005-397-26	US-08-903-800A-5	US-09-036-987A-1	-09	US-09-232-191-30	US-09-232-200-80	US-09-232-197-80	US-09-232-201-80	US-08-724-394A-20	US-08-724-394A-21	US-08-724-394A-22	US-08-998-416-1046	US-09-315-793-61	US-08-985-950-5	US-08-985-950-7	US-08-551-459-3	-459-	US-09-042-353-251	Ā	-08-053-131-1	US-08-645-641-134	US-07-853-408B-134	US-08-096-762-134
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228 229 333 333 24 44 54 54 54 55 55 55 55 55 55 55 55 55
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## ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Delcuve, Genevieve
APPLICANT: Awang, Gregor
TITLE OF INVENTION: Recombinant DNA Molecules and Expression
TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURTAIN APPLICATION DATE

CURTAIN APPLICATION NUMBER: US/08/083,795A
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 7841-062
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 364-7311
TELEPAN: (416) 361-1398
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 2529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                          ; Sequence 37, Application US/08883795A ; Patent No. 5985607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE:
; CLONE: Rh 10
US-08-883-795A-37
                                                                                                                                                                                                                                                                                                                   STATE: Ontario.
COUNTRY: Canada
ZIP: MSH 3Y2
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
RESULT 1
US-08-883-795A-37
                                                                                                                                                                                                                                                                                                CITY: TOR
STATE: OR
COUNTRY:
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Gaps ó; 33.1%; Score 23.8; DB 2; Length 2529; 59.7%; Pred. No. 2.3; tive 0; Mismatches 27; Indels 0 Query Match 33.1 Best Local Similarity 59.7 Matches 40; Conservative

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CORRESPONDENCE ADDRESS
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PCT-US95-06815-1
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           Gaps
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tive 0; Mismatches 18; Indels 0;
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                                                                                                                                                                                                                                                 APPLICANT: Fu, Ying-Hui
APPLICANT: Fu, Chang-En
APPLICANT: Vu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Oshima, Junko
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104-7092
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC 1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9506815
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                              RESULT 2
US-08-781-891-79/C
Sequence 79, Application US/08781891
; Patent No. 6090620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 87350 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity 65.49
Matches 34; Conservative
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TITLE OF INVENTION: PITILE OF INVENTION: AN NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Washington
                                                                                                                       1067 CCCAAAA 1073
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US-08-781-891-79
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                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06815
FILING DATE: 31-May-1995
Novo Nordisk of North America, Inc.
ADDRESSEE: Novo Nordisk of North America STREET: 405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                                                                                                                                                                     NAME: LOWINGY, KAITEN A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4184.204-WO
TELECOMMUNICATION INFORMATION:
TELETERIONE: 212 867 0123
TELETERIONE: 212 867 0124
TELETERIONE: 312 867 0124
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3187 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Myceliophthora thermophila
                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/253,781
AFILING DATE: 03-20ne-1994
ATTORNEY/AGENT INFORMATION:
NAME: LOWNEY, Karen A.
                                                           ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
US-08-706-037-26
Sequence 26, Application US/08706037
Patent No. 5770419
GENERAL INFORMATION:
APPLICANT: Xu, Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
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833...917
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Best Local Similarity
Matches 35; Conserv
                                       RY: U.S.A.
10174-6401
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CITY: I
STATE:
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APPLICANT: Berka, Randy M.

APPLICANT: Wahleithner, Jill A.

APPLICANT: Wahleithner, Jill A.

TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTS WITH

TITLE OF INVENTION: BNHANCED ACTIVITY

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 57704190 No. 5770419disk of No. 5770419th America, Inc.

STREET: 405 Lexington Avenue, 64th Floor
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Patent No. 5972670
GENERAL INFORMATION:
APPLICANT: Eerka M. APPLICANT: Berka, Randy M. APPLICANT: Berka, Randy M. TITLE OF INVENTION: BLUE COPPER OXIDASE MUTANTILE OF INVENTION: ENHANCED ACTIVITY
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,037
FILING DATE: 30-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION:
FILING DATE: 30-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATE:
APPLICATION DATE: US 60/002,800
FILING DATE: 1-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: HARTINGTON, James J.
REGISTRATION NUMBER: 38,711
REGISTRATION NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 45.26.200-U.
TELEPHONE: 212-867-0123
FELEPHONE: 212-867-0123
FILEPHONE: 212-867-0123
FILEPHONE: 212-878-9555
FINFORMATION FOR SEQ. ID NO: 26:
SEQUENCE CHARACTERISTICS:
FONCTH: 3192 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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US-08-706-037-26
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US-09-005-397-26
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Db 1545 GCCTCGCTGCCGTACCACCTGGGTGTGTTCCCCATCAGCGACTACTACT 1599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 31.9%; Score 23; DB 2; Length 3192; Best Local Similarity 63.6%; Pred. No. 5.2; Matches 35; Conservative 0; Mismatches 20; Indels
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin_Release #1.0, Version #1.30
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STREET: Keukdong Villa Ka-101, Kwangjang-dong,
STREET: Kwangjin-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Republic of Korea
ZIP: 143-210
SIPSESSE: CHOI, Bui-Sung
STREET: Dasol Apt. 102-507, #395-3, Kung-dong,
                                                                                                                                                                                                                                                                              PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRILING DATE: 30-AUG-1996
APPLICATION NUMBER: US 60/002,800
FILING DATE: 1-SER-1996
ATTORNEY/AGBWT INFORMATION:
NAME: HAITINGTON, James J.
RECISPERNCE/DOCKET NUMBER: 38,711
REFERENCE/DOCKET NUMBER: 38,711
REPERENCE/DOCKET NUMBE
                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08903800A Patent No. 5935789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 3192 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: FITTE OF INVENTION: FITTE OF INVENTION: FITTE OF INVENTION: TITLE OF INVENTION: T
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US-08-903-800A-5/C
                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION:
; LOCATION:
US-09-005-397-26
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GENERAL INFORMATION:
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                                 E: KIM, Chul-Ho
Shindonga Apt. 2-1101, Yongjeon-dong, Dong-gu
                                                                                                                                                                                                                                                                                           ADDRESSEE: KANG, Hyun-Ah
STREET: Kyungseong Keunmaul Apt. 125-1501, Kalma-dong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dehydrogenase gene of Hansenula polymorpha DL-1(ATCC 26012)
                                                                                                                                                                  ADDRESSEE: SOHN, Jung-Hoon
STRREET: Nuri Apt. 103-506, Wolpyung-dong, Seo-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette, 3.5inch, 1.44MB storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: glyceraldehyde-3-phosphate OTHER INFORMATION: dehydrogenase gene of Hanse OTHER INFORMATION: polymorpha DL-1(ATCC 26012)
                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: KIM, Hwa-Young
STREET: #3-462, Bukahyun-3-dong, Seodaemun-gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/903,800A
FILING DATE: 31-JUL-1997
CTASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 97-3173
FILING DATE: 31-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                       : Daejeon
RY: Republic of Korea
300-200
                                                                                                                                                                                                                                         XY: Republic of Korea 302-280
Republic of Korea
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120-190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2375 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC/AT OPERATING SYSTEM: MA
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                                     ADDRESSEE:
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COUNTRY:
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; Sequence 1, Application US/09036987A; Patent No. 6143526

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Db 14307 TTGAGGTCGGGACGTCCGCAGCCGCGCGCACCACTCGGGAGGCCTGGAAGCC 14365
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APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
APPLICANT: Treadway, Patti J
CAPPLICANT: Treadway, Patti J
APPLICANT: Waldron, Clive
TILE OF INVEXTION: Biosynthetic Genes For Spinosyn Insecticide
FILE REFERENCE: 50489 DIVI
CURRENT APPLICATION NUMBER: US/09/370,700
CURRENT APPLICATION NUMBER: US/09/370,700
EARLIER PELING DATE: 1999-08-09
EARLIER PELING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                    APPLICANT: Treadway, Patti J.
APPLICANT: Turner, Jan R.
APPLICANT: Waldron, Clive
TITLE OF INVENTION: Biosynthetic Genes For Spinosyn Insecticide
TITLE OF INVENTION: Production
                                                                                                                                                                                                                                                                                                                                        SEE: Dow AgroSciences LLC Patent Department: 9330 Zionsville Road
Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/036,987A
APPLICANT: Baltz, Richard H.
APPLICANT: Broughton, Mary C.
APPLICANT: Crawford, Kathryn P.
APPLICANT: Madduri, Krishnamurthy
APPLICANT: Merlo, Donald J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 1, Application US/09370700
; Patent No. 6274350
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Stuart, Donald R
REGISTRATION NUMBER: 28,479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (317)337-4847 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80161 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Indiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                         usa
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US-09-232-197-80/c
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LENGTH: 1968
                                             1968
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                                                                                                                     DB 4; Length 80161;
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                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TILE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MB
CURRENT APPLICATION NUMBER: US/09/232,200A
CURRENT APPLICATION NUMBER: 05/09/232,200A
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
                                                                                                                   Query Match 30.8%; Score 22.2; D Best Local Similarity 61.0%; Pred. No. 30; Matches 36; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-232-200-80/c; Sequence 80, Application US/09232200A; Patent No. 6288213
                                           TYPE: DNA
CRGANISM: Saccharopolyspora spinosa
US-09-370-700-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-232-191-30
SOFTWARE: Patentin Ver. 2.
            SEQ ID NO 1
LENGTH: 80161
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Sequence 80, Application US/09232201A
Patent No. 634831
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Lodish, Harvey F.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gineno, Ruth E.
APPLICANT: Gineno, Ruth E.
APPLICANT: Gineno, Ruth E.
APPLICANT: Gineno, Ruth E.
FILE REFERENCE: WH197-21P3MC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTA ACID TRANSPORT PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT PELICATION NUMBER: US/09/232,197A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/232,201A CURRENT FILING DATE: 1999-01-14 EARLIER APPLICATION NUMBER: 60/011,374 EARLIER FILING DATE: 1998-01-15 EARLIER APPLICATION NUMBER: 60/093,491
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 80, Application US/09232197A Patent No. 6300096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Caenorhabditis elegans
US-09-232-197-80
                                                                                                    TYPE: DNA; ORGANISM: Caenorhabditis elegans
US-09-232-200-80
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Query Match
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                 0; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Feder, John N.
APPLICANT: Kronmal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolfi, Roger, Yenta
APPLICANT: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPRAN: 415-576-0200
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/110,941
BARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/08724394A Patent No. 5872237 GENERAL INFORMATION:
                                                                                                                                                  TYPE: DNA CRENOTHADDILIS elegans US-09-232-201-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: not relevant TOPOLOGY: not relevant
                                                                                                                                                                                                                                                           30.6%;
67.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08 FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 67.44
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                           SEQ ID NO 80
LENGTH: 1968
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                                                                                                                                DD 183607 GAAGACCCITATGTGTCITTCAACTCTCACATCTATTTAGATGCAATTGGAGTCCCACAG 183666
                                                                                                       9 gacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaacag 68
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Score 22; DB 2; Length 246240;
Pred. No. 50;
0; Mismatches 25; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1 TITLE OF INVENTION: Sequences and Antibodies Thereto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1..246240
OTHER INFORMATION: /note= "HLA-H.CONTIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     017957-000100
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 21, Application US/08724394A
; Patent No. 5872237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION UNDMER: 35,136
REFERENCE/DOCKET NUMBER: 0179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Feder, John N. APPLICANT: Kronmal, Gregory S.
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       30.6%;
ilarity 59.7%;
Conservative 0
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LENGTH: 246240 base pairs
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STRANDEDNESS: not r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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MOLECULE TYPE: CDNA
                              Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
94111-3834
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PREMIT 15

GENERAL INFORMATION:

MAPLICANT:

MAPLICANT
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

July 31, 2002, 12:11:57; Search time 5855.71 Seconds (without alignments) 165.954 Million cell updates/sec

US-09-899-718A-4 72 1 cctttcaggacgatgcttcg.....catgtgagcccaacagtggc 72 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

27472414 Total number of hits satisfying chosen parameters:

13736207 seqs, 6748477542 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

EST:* Database :

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em_esthum:*
em_estnu:*
em_estov:*
em_estor:*
em_estp:*
em_estro:*
em_htc:*
gb_est1:*
gb_htc:*
gb_htc:*
em_gss_hum:*
em_estba:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	TOTO AT TORDA	AQ466003 HS_5139_B	BE750138 201331 MA	BF028674 601763910	BH103249 RPCI-24-2	BG676499 602622960	BG852601 1024034F0	BH176205 005_F_08-	AL613147 T7 end of	AL613148 T7 end of	AQ536358 RPCI-11-3	AW836780 QV1-LT003	AQ320218 RPCI11-10	AQ716839 HS_5473_A	BB524309 BB524309	BF143122 601788012	AQ785147 HS_3159_A	BH210823 Sm1-60D24
	Ţ		AQ466003	BE750138	BF028674	BH103249	BG676499	BG852601	BH176205	CNS07J0P	CNS07J0Q	AQ536358	AW836780	AQ320218	AQ716839	BB524309	BF143122	AQ785147	вн210823
	g	9 ;	12	10	10	12	10	10	12	12	13	12	σ		12		10	12	13
	Query	יייין ליייי	450	544	877	340	930	2069	305	305	305	447	557	622	502	273	625	510	555
æ	Query	March	37.8	37.5	37.5	37.2	36.7	36.7	36.1	36.1	36.1	36.1	36.1	36.1	35.8	35.6	35.6	35.3	35.3
	arcos	acore.	27.2	27	27	26.8	26.4	26.4	26	56	26	26	26	26	25.8	25.6	25.6	25.4	25.4
	Result	NO.	c 1	7	с С	4	ß	9	c 7	8 0	o 0	10	11	12	13	c 14	15	16	17

7 AZ941767	BB483511 I	AQ297755		AZ230592		9	AV336150	BE140819		AA169000	AU179961 P		BM253384		BF725277	EQ.	BJ020917	4 BF664154	1 BG484311 60250494	2	0	BF955906	BE524520	AZ111630	AZ951598	4 AZ496954	22 RH211493 Sm1-541,5
AZ94176	BB483511	AQ297755	AQ005736	AZ23059	BE854968	BF183196	AV336150	BE140819	AI592234	AA169000	AU179961	AQ433466	BM25338	AQ72250	BF725277	BB322109	BJ02091	BF664154	BG48431	BG331922	R56980	BF955906	BE524520	AZ11163	AZ951598	AZ49695	BH21149
12	6	12	12	12	10	10	6	6	σ	6	6		0	N				10	10	10	10	10		12		12	12
581	285	413	471	482	127	193	235	253	270	394	465	518	576	620	636	673	674	747	769	1161	152	231	406	635	642	661	663
35.3	35.0	S	35.0	S	4	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.7	34.4	34.4	34.4	34.4	34.4	34.4	34.4
25.4	25.2	25.2	25.2	25.2	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	24.8	24.8	24.8	24.8	24.8	24.8	24.8
18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	36	40	4.1	42	43	44	4.5
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## ALIGNMENTS

AQ466003  HS_5139_B2_E07_SPGE RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=715 Col=14 Row=J, DNA sequence.  AQ466003  AQ466003.1 GI:4643098 GSS. 23-APR-1999  AQ466003.1 GI:4643098 HOMO sapiens  HOMO sapiens	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 450) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589  Contact: Mahairas GG. Wallacc JC, Hood L High Throughput Sequencing Center Indh Throughput Sequencing Center Onlowersity of Washington and A01 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887  Email: jwallacceu.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC Library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from labrary availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from hattp://www.htsc.washington.edu http://www.htsc.washington.edu Plater: 715 row: J column: 14 Seg primer: SP6 Class: BAC ends	High quality sequence stop: 450. Location/Qualifiers 1. 450 /organism="Homo sapiens"
RESULT 1 AQ46603/C LOCUS DOETINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT	FEATURES source

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62.7%; Pred. No. 33; tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:3995858"
/clone_lib="NIH_MGC_53"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                        BF028674.1 GI:10736386
                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                225 CCACCTG 231
                                                                                                                                                      62 ccaacag 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                          42;
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                                                                                             Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at CORI sites.

126 g LOSR sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 544)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.W., Rohrer.G.A., Chitko-WcKown,C.G.,
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 25-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence evaluation of four pooled-tissue normalized bovine cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 20 and day 40
                                                                               /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                 374 TCTCAGGAAAATACTTCTAAGTGCCTAGCACAGGGTTTAGCACATTG 319
                                                                                                                                                                                                                                                                                                                                                       3 tttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtg 58
                                                                                                                                                                                                                                                                     37.8%; Score 27.2; DB 12; Length 450; 67.9%; Pred. No. 27; tive 0; Mismatches 18; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                   /clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201331 MARC 4BOV Bos taurus cDNA 5', mRNA sequence.
BE750138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
NO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                 /clone="Plate=715 Col=14 Row=J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             544 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9913"
/clone_lib="MARC 4BOV"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: 110 row: E column: 20 Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT BACKWARD: GTTTTCCCAGTCACGACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae; Bos.
                                                              /sex="male"
                                                                                                                                                                                                                                                                                         Best Local Similarity 67.99
Matches 38; Conservative
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37.5%; Score 27; DB 10; Length 544;

Query Match

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BF028674 877 bp mRNA linear EST 10-OCT-2000 601763910F1 NIH_MGC_53 HOMO sapiens CDNA clone IMAGE:3995858 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site_1: Sill (ggccgcctcggcc); Site_2: Sfil (ggccattatggcc); Double-stranded cDNA was prepared from cell line RNA.); Double-stranded cDNA was prepared from cell line RNA. S' and agaptors were used in cloning as follows: S' adaptor sequence: 5'-AKGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCGGAGGGGGCGAATG-dI(30)BN-3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where B = A, C, or G and N = A, C, G, or T). Average insert size 1.55 kb (range 0.94.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for Lull-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM847 row: d column: 03
                                                                                                               165 CCTGCTGGCAGGTGCCACCTGAGCTTTGACCCATCCGTTCGGATCTCTGACATCTGACC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                   2 ctttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagc 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="carcinoma, cell line"
/lab_host="DH10B (Tl phage-resistant)"
/note="crgan: bladder; Vector: pDNR-LIB (Clontech);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.5%; Score 27; DB 10; Length 877; 62.7%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Indels
25; Indels
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/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db.xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="squamous cell carcinoma"
/lab_host="DHIOB (TI phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.

1 (bases 1 to 2069)
Grossman, A., Daryles, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Unpublished (2000)
Contact: Charles Hauser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG852601 2069 bp mRNA linear EST 29-MAY-2
1024034F08.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM10598 row: h column: 15
High quality sequence stop: 842.
Location/Qualifiers
1 (bases 1 to 930)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Trissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 63;
0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:4747838"
/clone_lib="NCI_CGAP_Skn4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
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65.0%;
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2 and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Labo, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Mussell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end age: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 230 row: C column: 14 Seg primer: SP6 Class: BAC ends.
                                                                                                                BH103249 340 bp DNA linear GSS 19-JUL-2001
RPCI-24-230C14.TJ RPCI-24 Mus musculus genomic clone RPCI-24-230C14
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 340)
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Best Local Similarity 68.5%; Pred. No. 34;
Matches 37; Conservative 0; Mismatches
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/clone="RPCI-24-230C14"
/clone_lib="RPCI-24"
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                                                      RESULT
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/note="Vector: pBluescript II SK-; Site_1: ECORI; Site_2: Mobil: This library, constructed by John Davies and Jeffrey McDermott, combines cDNAs from CC-1690 cells grown to mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in ambient levels of CC2 and HS medium bubbled with 5% CC2. PolyA mank was purified from each sample, pooled and cDNA synthesized: The cDNA was directionally cloned into lambda ZAP II (Stratagene) in the ECORI (5') and XhoI (3') sites.
                                                                                                                                                                                                                                                                                   ZAP clones by superinfection with ExAssist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al (1996) Genome Research 6: 791-806." 559 c 637 g 275 t 61 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   005_F_08-21 SmBAC1 Schistosoma mansoni genomic clone 005F08 5', DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2017 CGATGCTCCGNCTGCTTGAGCCATCTATCTTTATGTAAANGACATCATCGAGTAAAGCGTG 1958
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to 305)
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al: (33) (0)3 20877783
ax: (33) (0)3 20877888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Indels
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/lab_host="Biomphalaria glabrata"
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/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially Hind III digested and size selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to Transform E. coli DH10B. The complete library contains 23808 clones from 4 independent
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Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeLoBAC II vector and used to transform E. coli DHIDs. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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DNA was ligated into Hind III digested pBeloBAC II vector and used
to transform E. coli DH10B. The complete library contains 23808
clones from 4 independent sizing-ligation-transformations. Average
insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
    GSS 08-OCT-2001
                   T7 end of clone 005DC04 of library SmBAC1 from strain Puerto-Rican of Schistosoma mansoni, genomic survey sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Williams, D.L., Johnston, D., LoVerde, P.T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
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                                                                                  AL613148.1 GI:16026354
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                                                                                                                               Schistosoma mansoni.
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                                                                                                                                                    Schistosoma mansoni
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                                                                                                                                 SOURCE
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-LT0036-150 200-070-f01st3=2000-02-15st4=1) Seq primer: puc 18 forward: High quality sequence start: 11 High quality sequence stop: 557.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW836780 557 bp mRNA linear EST 18-MAY-2000
OV1-LT0036-150200-070-f01 LT0036 Homo sapiens CDNA, mRNA sequence.
AW836780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 557)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

Library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: SP6

Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library"

10 91 c 100 9 115 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.1%; Score 26; DB 12; Length 447; 70.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 cttcggtgccttaagacacctacctttgtgtgtctatgacatgtgagcccaa 65
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Lymphocytes"
                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="RPCI-11-318M10"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .557
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GSS 13-JUL-1999

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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Queen Anne Avenue North, Seattle, WA 98109, USA
701 Closen Anne Avenue North, Seattle, WA 98109, USA
701 Fax: (206) 616-3887
702 Email: jWallace@u.washington.edu
702 Email: jWallace@u.washington.edu
703 Email: jWallace@u.washington.edu
704 Etere dejong.med.buffalo.edu/ordering_bac.htm)
705 Ficm Resear h Genetics (info@resgen.com). BAC end Web Server:
706 Primer: 77
707 Ender Now. Hisc. washington.edu
708 Primer: 77
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                             AQ716839 502 bp DNA linear GSS 13-JUL-HS_5473_Al_D10_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1049 Col=19 Row-G, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                   304 CTTTCATCACATAAGTCATCTACAGTTGTGTTTCTCACATGTGAGGTCAA 353
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                                                                                                                 16 cttcggtgccttaagacacctacctttgtgtctatgacatgtgagcccaa 65
                                                          15; Indels
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                                                      0; Mismatches
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                           Pred. No. 77;
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/db_xref="taxon:9606"
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Location/Qualifiers
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AQ716839.1 GI:5466155
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36; Conservative
                    Best Local Similarity 70.0 Matches 35; Conservative
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                                                                                                                    Once-Torgan: leiomios; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,
Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANJSUV218 622 bp DNA linear GSS 06-MAY-19:
RPCIII-100CI.TV RPCI-11 Homo sapiens genomic clone RPCI-11-100C1,
DNA sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please context Pieter de Jong
(pleter@dejong.med.bufalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26; DB 9; Length 557;
Pred. No. 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone="RPCI-11-100C1"
/clone_lib="RPCI-11"
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                                                                 /clone_lib="LT0036"
/dev_stage="Adult"
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70.0%;
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Fax: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF143122 625 bp mRNA linear EST 24-OCT-2000 601788012F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4015898 5',
was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript \mathsf{KS}(+) after bulk excision from Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 625)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                              35.6%; Score 25.6; DB 9; Length 273; 59.7%; Pred. No. 84;
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Pred. No. 1.1e+02;
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/db_xref="taxon:10090"
/clone="IMAGE:4015898"
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Matches 34; Conserva
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci
, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
Hivozane, T., Hori, F., Ishi, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K.,
Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokata, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasuhishi, A., Yokata, T., Yamamura, T., Yamanaka, I.,
Yano, R., Yasuhishi, A., Yokata, T., Yoshino
RIKEN Mouse ESTS (Konno, H., et al.)
Unpublished (2000)
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UKL:http://qenome.gsc.riken.go.jp,
UKL:http://qenome.gsc.riken.go.jp,
N. okazaki, Y. Maramatsu, M. and Hayashizaki, Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh, M., Kisunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, W., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 273)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RIKEN full-length enriched, 15 days embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please visit our web site (http://genome.rtc.riken.go.jp) for
           BB524309 RIKEN full-length enriched, 15 days embryo head Mus musculus cDNA clone D930019D20 3', mRNA sequence.
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/dev_stage="15 days embryo"
/lab_host="DH10B"
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/db_xref="taxon:10090"
/clone="D930019D20"
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                                                                                             BB524309.1 GI:9575767
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                 DEFINITION
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JOURNAL
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COMMENT

FEATURES

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Gaps

Search completed: July 31, 2002, 12:12:01 Job time: 13474 sec

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GenCore version
Copyright (c) 1993 - 2000
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                            capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                          (ABB57137-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                         insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.6%; Score 25.6; DB 23; Length 3085; 59.7%; Pred. No. 3.7; Live 0; Mismatches 29; Indels 0;
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                                                               Claim 1; SEQ ID NO 1864; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3085 BP; 861 A; 776 C; 752 G; 696 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD, Myers EW;
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11-JUL-2000; 2000US-0614150.
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Matches 43; Conservative
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derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be 5' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs are also used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted protein; cDNA isolation;
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                                                                                                                                                                          specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 cetttcaggacgatgettcggtgcettaagacacetacetttgtgtetatgacatgtgag 60
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                      The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                 35.6%; Score 25.6; DB 23; Length 20261; 59.7%; Pred. No. 6.7; tive 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                            Sequence 20261 BP; 5591 A; 4571 C; 4371 G; 5728 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein 5' EST, SEQ ID NO: 12022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID 12022; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC07947 standard; cDNA; 152 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 17267 tecaaaagtgee 17278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 cccaacagtggc 72
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                                                                                              (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1033401-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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AAX13569 standard; DNA; 626

AAX13569/c

(first entry)

19-MAR-1999

AAX13569;

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Sequence 152 BP; 26 A; 48 C; 49 G; 29 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                   Gaps
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       Score 25; DB 21; Length 152;
Pred. No. 2.5;
0; Mismatches 15; Indels
                                                                                                                                                                                         caggacgatgcttcggtgccttaagacacctacctttgtgtctatgaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne Edwards J, Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein 5' EST, SEQ ID NO: 213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 213; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy; chromosome mapping; ss
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ID AAC00215 standard; cDNA; 424
       34.7%;
69.4%;
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Query Match
Best Local Similarity 69.44
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC00215;
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982 nucleotide sequences isolated from the Enterococcus facealis genome. AAX12938 to AAX13919 represent these nucleotide sequences also known as contigs. The computer-based system can identify fragments of the Enterococcus facealis genome with commercial importance. The products can be used to detect the presence of Enterococcus facealis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus facealis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus facealis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   computer readable medium has been developed which has recorded on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 626 BP; 183 A; 124 C; 126 G; 191 T; 2 other;
                                                              Enterococcus faecalis genome contig SEQ ID NO:632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 1880; 2084pp; English.
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                                                                                                                                                                                                                                                                             97US-0066009.
97US-0044031.
97US-0046655.
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                                                                                                                                                                                                                                             98WO-US08985
                                                                                                                                                Enterococcus faecalis
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Score 25; DB 21; Length 424; Pred. No. 3.4; 0; Mismatches 15; Indels

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Query Match Best Local Similarity Matches 34; Conserva

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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
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01-SEP-2000;
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18-AUG-2000;
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14-SEP-2000;
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25-SEP-2000;
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14-AUG-2000;
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30-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunosuppressive, antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antishematic; hepatotropic; cerebroprotective; antiinflammatory; antialiabetic; antiulcer; antiinflammatory; antialiabetic; antiulcer; antiinflammatory; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        acids derived from human pancreatic tumor tissue which have cytostatic activity. The sequences are also useful in producing pharmaceutical compositions for treatment of pancreatic tumors. AAZ52858-Z53014 represent expressed sequence tag (EST) fragments derived from a human pancreatic tumor cDNA library and which encode the proteins represented in AAY73814-Y74252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention describes novel polypeptides and their encoding nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                New human nucleic acid sequences from pancreatic tumors, and related
                                                                              Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                       Rosenthal A, Specht T, Hinzmann B, Schmitt A, Pilarsky C,
                                          Human prostate tumor cDNA library derived EST fragment #148.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25; DB 20; Length 907; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 CAGGAGGATTCGGGGCGCCATGACCCCCAACCTCCGCGTCTGGGAAA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caggacgatgcttcggtgccttaagacacctacctttgtgtctatgaca 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 907 BP; 152 A; 266 C; 323 G; 166 T; 0 other;
                                                                                                                                                                                                                                                                                                                                (META-) METAGEN GES GENOMFORSCHUNG MBH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Page 299-300; 502pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.78;
69.48;
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14-MAR-2000 (first entry)
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Best Local Similarity 69.4 Matches 34; Conservative
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                                                                                                    treatment; ds
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Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ruben SM;
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17-NOV-2000;
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The Thronicon retries of preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone home marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemaly autoimmune thyroiditis; diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoardial ischaemias; (d) wound healing; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                               The invention relates to novel genes (ABA11004-ABA21534) and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, prostate cancer antigen; cytostatic; uropathic; diagnositc, reproductive system; chromosomal marker; forensic; urinary disorder; chronic nephritis; blood-related disorder; thrombosis; ds.
                               Disclosure; SEQ ID NO 10456; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 34.7%; Score 25; DB 22; Length 3098; Best Local Similarity 69.4%; Pred. No. 6.4; Matches 34; Conservative 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human prostate cancer antigen, Seq ID No 573.
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cancers and metastases -
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-451929/48.

Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis  $\cdot$ 

Disclosure; SEQ ID No 573; 546pp; English.

The invention relates to novel isolated human prostate cancer antigen polynucleotides (I) and polypeptides (II). (I) and (II) are useful for preventing, treating or ameliorating a medical condition when administered. (I), (II) and the antibody to (II) are useful for treating, proventing and/ or prognosing disorders related to the reproductive system including prostate cancers; urinary disorders e.g. chronic nephritis; and blood-related disorders e.g. thrombosis. (II) can be used for testing and detection e.g. as a chromosomal marker and in forensics (I) and the anti-(II) antibody can be used in testing and detection in immunoassays. Assi0061-Ass40775 represent the human prostate cancer antigen coding sequences, and related PCR primers and sequences of the Invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format

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29-SEP-2000;
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directly from WIPO at: ftp.wipo.int/pub/published_pct_sequences.
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                                                               15; Indels
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                                           Score 25; DB 22;
Pred. No. 6.4;
0; Mismatches 15;
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2000US-020515.
2000US-021647.
2000US-021647.
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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cytostatic; gene therapy; vaccine; metastasis; ds.
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17-NOV-2000; 20000S-0249390.
01-DEC-2000; 20000S-0251988.
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05-DEC-2000; 20000S-0251856.
08-DEC-2000; 20000S-0251866.
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17-NOV-2000; 2000US-0249265.
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05-JAN-2001; 2001US-0259678.
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02-MAR-2000;
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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
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08-DEC-2000;
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Ruben SM; WPI; 2001-483426/52.

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AAK AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) aniho acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) toroteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectlifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) to polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK6750 and AAM82169 cepresent sequences used in the exemplification of the present invention.
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                         Disclosure; SEQ ID NO 41683; 3071pp + Sequence Listing; English.
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P-PSDB; ABB50296.
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                                                                                                                                                                                    The invention relates to methods for diagnosing and prognosing ovarian tumours in an individual via the detection and measurement of the expression of ovarian tumour marker genes (ABA83128-ABA83128), ABA83180, ABA83181, ABA83181, ABA83181, ABA83181, ABA83181, ABA83181, ABA83181, ABA83181, The methods of the invention are useful for detecting an ovarian tumour in a patient, for identifying an individual at increased risk for developing ovarian cancer, in prognostic tests for monitoring a patient in remission from ovarian cancer, in tests for monitoring a patient in remission from ovarian cancer. The methods can additionally be used to identify a particular tumour as being an ovarian tumour (i.e., an epithelial ovarian tumour selected from serious cystadenocarcinoma, proderline serous tumour, serous cystadenocarcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clear cell adenocarcinoma, cystadenofibroma, adenofibroma and Brenner tumour. The ovarian tumour marker genes of the invention were identified using SAGE (serial analysis of gene expression) and were found to be overexpressed in a broad variety of ovarian epithelial tumour cells relative to normal ovarian epithelial cells. The marker genes are implicated in immune response pathways, in the regulation of cell proliferation and in protein folding, and many of these are membrane-localised or secreted. In addition to their use as diagnostic and prognostic markers, the ovarian tumour marker genes or their encoded proteins may be used as therapeutic targets for the treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote- "Nucleotide R is present at this location in the sequence shown in sequence listing of the specification" 4067..4528
                 Detecting and identifying ovarian tumor, identifying increased risk for developing ovarian cancer, and determining effectiveness of ovarian cancer treatment, by measuring expression level of ovarian tumor marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mucinous cystadenoma, borderline mucinous tumour, mucinous
cystadenocarcinoma, endometrioid carcinoma, undifferentiated carcinoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevention of ovarian cancer. Sequences ABA83081-ABA83122, ABA83180, ABA83180 aBA83182 and ABA83184 represent the ovarian tumour marker genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human glutamate receptor, metabotrophic 3 (GRM3) gene fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.7%; Score 25; DB 22; Length 4316; 69.4%; Pred. No. 7.1; tive 0; Mismatches 15; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    873 CAGGAGGAGCTTCGGGGCGCCATGACCCCAACCTCCGCGTCTGGGAAA 825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4316 BP; 1000 A; 1090 C; 1292 G; 934 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nootropic; gene therapy; neurotransmitter; chromosome 7q; drug screening; neurological disorder; polymorphism; ds.
                                                                                                                                              Claim 23; Page 124-126; 140pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD26400 standard; DNA; 50000 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //oce "Nucleotide Y is present at this location in the
sequence shown in sequence listing of the specification"
26032..50000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Nucleotide M is present at this location in the sequence shown in sequence listing of the specification" % \left( \frac{1}{2}\right) =\frac{1}{2}\left( \frac{1}{2}\right) =\frac{1}
                                                                                  /note= "Nucleotide R is present at this location in the sequence shown in sequence listing of the specification'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide, a polymorphic variant of glutamate receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                   replace (25586, T)
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replace (4192, A)
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Matches 36; Conservative
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25176..
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                                                          '*tag=
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    variation
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Location/Qualifiers
                                                                                                                                                  Tanguay DA;
                                                                                                                                           (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                    16-JUN-2000; 2000US-212328P.
                                                                                                                             18-JUN-2001; 2001WO-US19447
      26-MAR-2002 (first entry)
                                                                                       (PS) 3"
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                                                         (PS) 1"
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25586
                                                                                           26157
                                                                                                                                                  Finkel K, Koshy B,
                                                                                                                                                          WPI; 2002-090198/12
                                                                                                              WO200196350-A2
                                     Homo sapiens.
                                                                                            misc_feature
                                               misc_feature
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                                                              misc_feature
AAD26437;
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polymorphic variant of glutamate receptor, metabofrophic 3 (GRM3)

sogene. GRM3 is a receptor for glutamate, the major excitory
isogene. GRM3 is a receptor for glutamate, the major excitory
recording contransmitter in the mammalian central nervous system. Human GRM3
located on chromosome 742.1-742.2 is expressed in human foetal and adult
whole brain especially in the caudate nucleus and corpus collosum. GRM3
control of GRM3. GRM3 polypeptide is used for screening drugs. A
recombinant non-human organism is used to study expression of GRM3 sG
in vivo, for in vivo screening and testing of drugs targetted against
compounds for neurological disorders in a biological system. GRM3
compounds for neurological disorders in a biological system. GRM3
compounds are for treating the efficacy of therapeutic agents and
compounds are for treating diseases associated with GRM3 activity,
e.g., neurological disorders. The present sequence is an allelic variant
of human GRM3 gene fragment containing polymorphic sites (PS).
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"This degenerate base represents polymorphic site
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"This degenerate base represents polymorphic site
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/note= "This degenerate base represents polymorphic site
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/note= "This degenerate base represents polymorphic site
Human GRM3 gene fragment #1 allelic variant containing polymorphic site.
                                                                                              Human; glutamate receptor metabotrophic 3; GRM3; neuroprotective; nootropic; gene therapy; neurotransmitter; chromosome 7q21.1-q21.2; drug screening; neurological disorder; polymorphic site; PS; ds.
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nucleic acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label cound to each probe of the microarray. The probes are useful for overlifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for gene discovery, and for determining predisposition and/or prognosing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical captures of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence data for this patent did not form part of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly printed.
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                 27892 AGGAACATGTTTTGGTTCCATAAAACACCTTGCAAAGGCTCTCTGAATTCTAAGC 27838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression in sample derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene pyracein in acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                   Human; microarray; single exon probe; gene expression; breast;
7 aggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for measuring gene expression in sample derived from breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 2605; 327pp + sequence listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                             Human breast cell single exon nucleic acid probe #2605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
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21-SEP-2000; 2000US-05346B7.
21-SEP-2000; 2000US-02346B7.
27-SEP-2000; 2000US-02356559.
04-OCT-2000; 2000GB-0024263.
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                                                                                                                                   ABA43910 standard; DNA; 479
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                                                                                                                                                                                                                                                                                                         disease; cancer; ss.
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                                                                                                                                                                         ABA43910;
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Gaps

Score 24.6; DB 24; Length 50000; Pred. No. 22; 0; Mismatches 19; Indels 0;

34.2%;

Query Match Best Local Similarity 65.5% ***^hes 36; Conservative

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Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
Human genome-derived single exon nucleic acid probes useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2668; 639pp + sequence listing; English.
                                                                                                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #2668.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           analyzing gene expression in human fetal liver
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                                                                                                                                                        ABA54363 standard; DNA; 479 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2000; 2000US-0207456.
30-UN-2000; 2000US-0608408.
03-AUG-2000; 2000US-0632366.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-0024263.
                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-2001; 2001WO-US00669
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                                                                                                                                                                                                                   01-FEB-2002 (first entry)
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                                             62 ccaacagtg 70
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DB 22; Length 479;

Ouery Match 33.6%; Score 24.2; Di Best Local Similarity 59.4%; Pred. No. 7.4;

41; Conservative

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62 ccaacagtg 70

CCCTGAGAG 4

2 ctttcaggacgatgcttcggtgccttaagacacctacctttgtgtctatgacatgtgagc 61

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Search completed: July 31, 2002, 14:11:17
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Gapop 10.0 , Gapext 1.0
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72
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Copyright (c) 1993 - 2000 Comp
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TITLE
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Sequence 4 from Patent W00202785.
AX349066
AX349066.1 GI:18615101
                                                                                                                                                               synthetic construct.
synthetic construct
artificial sequence.
                                                                                             Sprunck,S., Kluth,A., Becker,D., Luetticke,S. and Loerz,H. Promoters of gene expression in plant caryopses Patent: WO 0202785-A 4 10-ZAN-2002; Aventis CropScience GmbH (DE)
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                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="01igonucleotide"
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Aventis CropScience GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 100.0%; Score 72; DB 6; Length 72; I Similarity 100.0%; Prod. No. 1.1e-16; 72; Conservative 0; Mismatches 0; Indels
                               Submitted (16-JAN-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Lbaraki 305-8602, Japan
                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 147220)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                AP004636 147220 bp DNA linear HTG 17-. Oryza sativa chromosome 8 clone P0685B10, *** SEQUENCING IN
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1 from Patent W00202785.
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                Direct Submission
                                                                                                                                                                                                                                Oryza sativa (cultivar:Nipponbare) DNA, clone:P0685B10.
                                                                                                                                                                                                                                                       HTG; HTGS_PHASE2
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/db_xref="taxon:4565"
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* NOTE: This is a 'working draft' sequence.

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On Aug 15, 2001 this sequence version replaced gi:13162501.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62385 TCAACAGTGG 62376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                             62 ccaacagtgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 195979)
DOE Joint Comme Institute,
                                                                                                                                                                                                                                                             196599 bp
Homo sapiens chromosome 2 clone
SEQUENCE, 22 unordered pieces.
ACO37494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (23-AUG-2001) DOE Joint Genome Institute, 2800 M: Drive, Walnut Creek, CA 94598, USA On Aug 23, 2001 this sequence version replaced gi:11079405 Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
                                                                                                          1 (bases 1 to 196599)
Birren, B., Linton, L., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STS Content:
SHGC-103233 G57536
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Quality: Phrap Quality >=40 99.5% of Sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOE Joint Genome Institute and Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-NOV-2000) DOE Joint Genome Institute, Drive, Walnut Creek, CA 94598, USA 5 (bases 1 to 195979)
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DOE Joint Genome Institute.
                                                                      Unpublished
                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHGC-78846 G48644.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            www.jgi.doe.gov
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                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                          AC037494.3 GI:10047908
                                                                                             Homo sapiens chromosome 2,
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                                                       (bases 1 to 196599)
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/db_xref="taxon:9606"
/chromosome="5"
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Pred. No. 3.7;
0; Mismatches
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                                                                                             aum, C. and Lander, E. clone RP11-528K12
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                                                                                                                                                                                                                                                                                               RP11-528K12
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Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Coyette,M., Graham,L., Galagan,J., Gardyna,S., Ginde,S., Coyette,M., Graham,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 182545 bases at least Q40
Consensus quality: 189073 bases at least Q30
Consensus quality: 19263 bases at least Q20
Insert size: 208000; agarose-fp
Insert size: 194499; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 4.3 in Q20 bases; agarose-fp Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center clone name: 528_K_12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L9640
                         25372 25471: gap of 100 bp
25472 31306: contig of 5835 bp in length
                                                                                                    22238 22337:
22338 253
   31307 31406:
                                                                                                                                                                  18393 18492: gap of 100 bp
18493 22237: contig of 3745 b
                                                                                                                                                                                                                                                                              14841 14940:
                                                                                                                                                                                                                                                                                                                                              11862 11961:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5531 5630; gap of 100 bp
5631 7168: contig of 1538 bp in length
7169 7268: gap of 100 bp
7269 8574: contig of 1306 bp in length
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                                                                                             337: gap of 100 bp
25371: contig of 3034 bp in length
                                                                                                                                                                                                                    18392: contig of 3452 bp in length
                                                                                                                                                                                                                                                                                                          14840: contig of 2879 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5530: contig of 5530 bp in length
   gap of
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82176 82275: gap of 25852 bp in length
108128 108127: gap of 100 bp
108128 108227: gap of 17038 bp in length
108228 125265: contig of 17038 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145215 145314: gap of 100 bp
145315 161113: contig of 15799 bp in length
161114 161213: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125266 125365: gap of 100 pp
125266 145214: contig of 19849 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183804 183903: gap of
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50747 58275: contig of 7529 bp in length
58276 58375: gap of 100 bp
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36290 36389; gap of 100 bp
36390 42370; contig of 5981 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69447 69546:
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42471 50646: contig of 8176 bp in length
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8675. .9935
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546: gap of 100 bp
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                                                                                                           Bowle, S., Briewa, M., Brown, E., Brown, M., Bryant, N.P., Burach, P., Burch, P., Carron, T.F., Carter, M., Cavacos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delagado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delagado, O., Dany, C., Dindy, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Eacotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, K., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Khan, U., King, L., Korvah, J., Johason, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Kovat, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, C., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lurder, A., Lucler, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martindale, A., Martindale, A., Mandale, P., Martin, R., Martindale, A., Nohabbat, K., Mosey, M., Nel, P., Martindale, A., Nohabbat, K., Mosey, M., Nel, P., Martindale, A., Payton, B., Peeter, J., Pickens, R., Primus, E., Pu, L., Peeter, J., Pickens, R., Primus, E., Pu, L., Peeter, J., Pickens, R., Paren, A., Tamerisa, K., Stone, H., Sthoshtari, N., Stone, R., Pate, A., Tamerisa, A., Tamerisa, A., Tamerisa, A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Norway rat.
Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC097952.2 GI:17948834
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62063 a
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norvegicus clone CH230-127L5, *** SEQUENCING IN PROGRESS
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                            Vasquez,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                   Vera, V., Villalon, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 196599;
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                                                                                                    Tamerisa, K.,
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:16327658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G. and Gibbs,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank.draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 63 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 134713 bases at least Q40
Consensus quality: 142480 bases at least Q30
Consensus quality: 148683 bases at least Q20
Estimated insert size: 145761; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------Project Information
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8720 bp DNA linear PRI 18-SEP-Bomo sapiens chromosome 2 clone RP11-569P21, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                 Drafting center: WIBR
                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                                                                                                                             Contact: submissions@watson.wustl.
                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
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On Sep 18, 2001 this sequence version replaced gi:7331466
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Waterston, R.H.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8720)
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                                                                                                                                                                                                                                                                                          3 tttcaggacgatgcttcggtgccttaagacacctacctttgtgtgtctatgacatgtg 58
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                        HTG;
                                                                       Norway rat.
                                                                                                        AC095124.2 GI:17942027
                                                                                                                                                            Rattus norvegicus clone CH230-8N7,
                                                                                                                                                                                 AC095124
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Submitted (23-OCT-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Oct 20, 2001 this sequence version replaced gi:14916246.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (19-JUI-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                         46 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
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Submitted (20-OCT-2001) Genome
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AC092662.2 GI:16303564
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COMMENT

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Center project name:

Project Information

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/cenbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 46 contigs. The true order of the pieces is not known and their order in this sequence record is

Consensus quality: 80643 bases at least Q40 Consensus quality: 86605 bases at least Q30 Consensus quality: 91484 bases at least Q30 Estimated insert size: 80824; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.5x in Q20 bases; sum-of-contigs estimation

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REFERENCE
AUTHORS
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Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J.,
Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kurceshi, A., Landry, N., Leal, B., Lewis, L. C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R. J., Lu, X., Lucler, A., Lucier, R., Luna, R.,
Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A.,
Martinez, E., Massey, E., Mawhiney, E., McLeod, M. P., Meador, M.,
Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K.,
Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N.,
Nguyen, A., Nguyen, N., Oyledo, R., Pace, A., Payton, B.,
Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L.,
Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M.,
Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N.,
Stone, H., Sutton, A., Syatek, A., Tabor, P., Tamerisa, K.,
Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R.,
Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C.,
Walliams, G., Williamson, A., Wleczyk, R., Wooden, S.,
Wainstock, G., and cibbs R.
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E Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Burch, P., Burkett, C., Burnell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy, Carroll, L., Deerich, D., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Daqber, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Harnlandez, T., Hernandez, O., Hodgson, A., Hodgson, M., Haylak, P., Hawes, A., Hernandez, T., Hernandez, O., Hodgson, A., Hodgson, M., Haylak, P., Hawes, A., Hernandez, M., Hernandez, O., Hodgson, A., Hodgson, M., Haylak, P., Hawes, A., Hernandez, O., Hernandez, O., Hodgson, A., Hodgson, M., Haylak, P., Hawes, A., Hernandez, O., Hernandez, O., Hodgson, A., Hodgson, A., Hodgson, M., Haylak, P., Hawes, A., Hernandez, O., Hodgson, A., Hodgson, A.
                                                                                                                                                                                                                                                                                               Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15625678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help6bcm.tmc.edu
                                                                                                                                                                                                            Center: Baylor College of Medicine

    Genome Center

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* arbitrary. Gaps between the contigs are represented as 
* runs of N, but the exact sizes of the gaps are unknown. 
* This record will be updated with the finished sequence
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                                                                                                                                                                                                                                              Oryza sativa genomic DNA, chromosome 1, PAC clone:P0043B10.
AP003236
                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                     Oryza sativa
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                                                                                                                                                                                                                                   AP003236.3 GI:15528647
                                                                                                                                                                                                                                                                  AP003236
     on Sep 7, 2001 this sequence version replaced gi:14149142. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTN2.0 as well as SplicePredictor
                                   Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                               published Only in Database (2001) In press 2 (bases 1 to 167399) Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                           Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
                                                                                                                                        Oryza sativa nipponbare(GA3) genomic DNA,
                                                                                                                                                   Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                        Direct Submission
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/db_xref="taxon:10116"
/clone="CH230-8N7"
/ 20865 c 20727 g 28460 t
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A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0043B10 clone has an overlap with P0560B06 clone (DDBJ: AP0032B1) at the position 1 to 117,634 of 5' end and an overlap with P0493G01 clone (DDBJ: AP002914) at the position 118,594 to 167,399 of 3' end. The sequence of this clone starts at the position 44,087 of P0560B06 and ends at the position 48,806 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN 2.0 with the
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complement(10234..11904)
/gene="P0043B10.2"
                                                                                                                                                                                                                             YGVGVDLWSAGCILAELLHGKPIMPGRTEVEQLHKIFKLCGSPSEEYWKKSKLPHATI
FKPQQPYKRCIREAFKDFPPSSLPLVETLLAIDPAERQTATSALQSEFFATEPYACDP
SSLPTYPPSKEMDAKMRDEEARRLRAAAKAKGEGVKRTRTRDRSQRAGPAPEANAELQ
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18162...18262,19937...20054,20838...21152)

/gene="pool43B10.3"

join(13564...13875,14001...14285,14372...14689,17077...17304,

18162...18262,19937...20054,20838...21152)
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/gene="P0043B10.1"
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/db_xref="taxon:4530"
/chromosome="1"
                                                                                                                                              QKGSSQTWSGPLVDPAALGQSRRKKQTALDAKAAAYSKQLQKDKGGTRAR"
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LEGLVTSRMSCSLYLVFEYMEHDLAGLAASPDVKFTLPQIKCYVQQLLSGLEHCHNNN
VLHRDIKGSNLLLDNNGILKIADFGLATFFDPRHKRPMTSRVVTLMYRPPELLLGATD
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/db_xref="GI:15528648"
/translation="MGCVFGRPSSSPPAAAARKGRRKKRSSPMPAPSTDSPAADQSPG/translation="MGCVFGRPSSSPPAAAARKGRRKKRSSPMPAPSTDSPAADQSPGRRPRRRIGRKPGPRQGCVPAPAAAEQLAAGWPPWLVAVAGEALRGWTPRRADTFEKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="P0043B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa"
                                                       Join(24290. .24311,24605.
/gene="P0043B10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="contains ESTs C74868(E60528),AU031247(E61207)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="P0043B10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /pseudo
/gene="P0043B10.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene≖"P0043B10.3"
                                   24311,24605.
                                   .24781,25674. .25883,27639.
                                                                                                              .24781,25674.
                                                                                                              25883,27639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cogon
                                                                                                              .27823)
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RLISOPSCIKGKMEDYQLAGLIMUIRLYENGINGILADEMGLGKTLQTISLLGYLHEF
RGITGPHMYVAPKSTLGNNIKEIORFCPILRAVKFLANKELAPEGKHUYC
VTSFEMAIKEKTTLKERSWRYIIDEMFCPILRAVKFLANKERHHIRENLLOPGKFDVC
VTSFEMAIKEKTTLKERSWRYIIIDEMFGIKNENSLLSKTMRIYNTWIRLIITGTPLO
NNLHBLMSLLNFLLEFISSAFITDEMFGISGENDQEVVQQLHKVLRPFLLRLKSD
VERGLPFKEFTILKVGMSOMGKOYYRALLOKDLEVINAGGERKRLLNIAMQLRKCCNH
PYLFGGAEBGPPYTTGEHLVENAGKMYLLDKLLPKLKDRDSRVLIFSOMTRLLDILED
YLMYRGYOYCRIDGNTGGEDRDASIEAFNKFGSSKFVFLLSTRAGGIGINLATADVVV
LYDSDMNPQADLQADDRAHRIGQKKEVQVFRFCTEYTIEEKVIERAYKKLALDALVIQ
QGRLAEQKTVNKDDLLQMVRFGAEMVFSSKDSTITDEDLDRIARAKKLANDANVIEPP
RGFERKRNYSESEYFKQALRQGAPAKPREDRIPRMPHLHDFQFFNNQRLNELYEKEVRY
LMQANGKKOTIDGEDEDOLEPLTABEQGEKEQLLEEGFATMFRRDENTFIRACEKYGR
KTTEDGLARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(30141. .30161,30286. .30396,30997. .31212, 31293. .31471,31621. .31786,31880. .31938,33031. .32073, 32251. .32320,32424. .32513,32587. .32708,32743. .32774, 32842. .33030,33114. .33207,33291. .3378,33464. .33684, 33890. .33963,34047. .34329,34421. .33578,33464. .34908, 34995. .35174,35271. .35368,35488. .35600,36122. .36225, 36366. .36488,36823. .37158))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(30141. 30161,30286. 30396,30997. 3121:31293,31371,31621. 31786,31880. 31938,2031. 32073,32251. 33320,33244. 32513,32587. 32708,32743. 32774,32842. 33303,33114. 33207,33291. 33378,33464. 33684,33890. 33563,34047. 34329,34421. 34555,34687. 34908,34995. 33574,35271. 35368,35488. 35600,36122. 38225,36366. 36488,36823. 37158))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GPNQDLLQVYFYLTTSLLVHRRQEMKFYTFWIRIRTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(37610. .37736,37900. .38138))
/gene="P0043B10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLSIVDHAGFHKFCDVLQPLFKLMSRNTIRKDILEVLTWVKEKRPSVTNTWMIKEVDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mrprkrgtpvTtpnTnSkDTnvIEIDDDVAVGnKrKLKYAIWQE
FGQVKVGNVWKAKCSWCQKLLSGNSGGCPHHSVMLETHVFDQNLARKKLALMICLHEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probably
                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MTSNVSIQDGPTATNRGLGPFVGRTRMQNLVEPNRLRPVRTDPNPKSAGGMPQTHPRLVGGNGAPPTSLLLNTLRTRGLRLRSAMKALPLLPLVVFLFETDISFAAVLEDFVAKPENFMEN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(37610. .37736,37900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFRFDWFYKSRTTQELARRCDTLIRLYEKENQEYDEQERQARKDKRWAKNMTPTKRSF
LRVSEGETTPSNSFKRRRQSLMDDYYGSGRRKRG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NDIRSIAAEMEGKTEEEVQRYAKVFKERYKELSDYDRIIKNIERGEARISRKDEIMR#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LKYLLQQTEIFAHFAKGNQSKEKKPRGRGRHASKMTEEEEDEEYLKEEEDALAGSGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VVGEDDDADEAEGGAVVGKREKARLKEMQKLKKQKIQEILDTQNAAVDADMNNKGKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAGEAAGGEEEEVDEEEIEAVTTGAGADEEEEESGAAAAAPGEGDEESQSTEDDEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="putative DNA-dependent ATPase"
/protein_id="BAB64717.1"
/db_xref="GI:15528650"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0043B10.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="hypothetical protein
/translation="maglaaarelrreglDVTVLEQSADVGGQWLYDAATDGRDPLGM
AGVHSSIYSSLRLNSPREVCGFSDFPFRPTNGGGGDARRYPVHGELLRYIREFCDVFG
                                                                                                                                                                                     similar to Arabidopsis thaliana chromosome 5, MXM12.4"
                                                                                                                                                                                                                                                                 join(39502. .40202,40249. .40864)
/gene="P0043B10.7"
                                                                                                                                                                                                                                                                                                                      /gene="P0043B10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="contains EST C74714(E50551)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein_id="BAB64718.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | IGKKLDRYKNPWLELKIQYGQNKGKFYNEECDRFMLCMYHKLGYGNWDELKAAFRMSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translation="MAKPVKYDEEEEEVSSSGEEEEEQSDGAGSGSGEEEDEEEEEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                        /protein_id="BAB64719.1"
/db_xref="GI:15528652"
                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                             note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="GI:15528651"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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gene CDS

gene CDS

LMDAVRLDTTVVRVAMAPPRRDGSLRWTVRSKHNGDAETEEVFDAVVVATGQYSQPRL

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RESULT 1
AP002914
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                   On Mar 28, 2001 this sequence version replaced gi:11191987. Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against work the sequence was searched against the sequence was sequence was sequenced to sequence was sequenced the sequence was sequenced to sequenced the sequenced to sequence was sequenced to sequenced the s
                   RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent the identified cDNA sequences using BASTN.2.0 with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-NOV-2000) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sasaki, T., Matsumoto, T. and Yamamoto, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (cultivar:Nipponbare) DNA, clone:P0493G01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AP002914.2 GI:13486690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa genomic DNA, chromosome 1, PAC clone:P0493G01.
corresponding DDBJ accession no. and RGP clone ID
                                                                                                                                                                                                                                      NCBI NonRedundant Protein database, nr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 167587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (sites)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                     /ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(47257. .47309,47457. .47625,47935. .48079,48190. .48309,
48945. .49010,50162. .50349)
/gene="p0043B10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similar to Oryza sativa chromosome 3, OSJNBa0040E01.24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (43356.
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complement//
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APSLSFYGIPYKYILPRFAEYQARWYAQYLSGRRTLPSPGEMLRAYEEYNRAKEAAGL
PKRQTHDLFLDLEYCDEYGERHCGFPRTEQWKKELIWSSISDMCDDIENFRDDYHDSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MRMAASGLSPLSQGRMKSQTRCPSPTGGYGTSTLNLAGVAGAVE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB64721.1"
/db_xref="GI:15528654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48945. .49010,50162. .50349)
/gene="P0043B10.9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LHYCPSSYNDFLAMVAMKPGMYLAGADVPTPGVPTPAPARDECLEALIIPTGRGEACV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="G1:15528653"
/translation="MGHTNLHSAGSRCNVEARLFADDATGVRPVTDRSFLSTTCQFSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSIDGMDKWRRRQLHSHSYRVPDSFAGEVVVIVGCNLSGKEVALELLRVAKEVHLSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oin(47257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     id="BAB64720.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .47309,47457. .47625,47935. .48079,48190. .48309,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167587 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8; Length 167399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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FEATURES
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                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                          misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GanomeSeq.html.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
probably inactive due to no initiation probably inactive due to stop codon(s)
                                                                                                               49182.
                                                                                                                                                                                                                                                       complement(34417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(28447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STTVR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHLARNPFGEIPVLEDGDLTLYQSRAIARYIFRKYKPEFLGLGEGGSLEESAMVDVWL
DVEAHQHEAAVRPILWHCIINKFEGRDRDQGVVDESVRKLEKVLGVYEARLSGSRYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="contains ESTs
AU031696(R0596),C97559(C60386),C28218(C60386),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(5920. .6398,6616. .6664,6958. .7107))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(5920. .6398,6616. .6664,6958. .7107))
                                                                                                                                                                                                     /gene="P0493G01.5"
/note="power-".
                                                                                                                                                                                                                                                          /gene="P0493G01.5"
complemen+''''
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="p0493G01.4"
/note="prober"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(28447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (20654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDRISLADLSHFSNMRYFMATEYAGVVDAYPHVKAWWEALLARPTVQKVMAGMPPDFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="putative glutathione S-transferase"
/protein_id="BAB39927.1"
/db_xref="GI:13486691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D28287 (R0596)
                                                                                                                                                                          pseudogene, mutator-like transposase'
                                                                                                                                                                                                                                                                                                                                                                       pseudogene, 12-oxophytodienoate reductase OPR2'
                                                                                                                                                                                                                                                                                                                                                                                                                            probably inactive due to no initiation/termination codons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(20654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pseudogene, 12-oxophytodienoate reductase OPR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="P0493G01.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="P0493G01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4530"
/chromosome="1"
                                                       /note="probably inactive due to frameshift(s) in CDS
                                                                                        /gene="P0493G01.6"
                                                                                                                                                                                                                                                                                                                                            /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="P0493G01.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="P0493G01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0493G01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="BAB39928.1"
/db_xref="GI:13486692"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="contains EST D15357(C0514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="P0493G01.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="P0493G01.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MAPMKVYGWVVSPWMARVLVALEEAGAEYEVVPMSRSGGDHRRP/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="P0493G01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Oryza sativa"
                                                                                                                                                                                                  'note="probably inactive due to frameshift(s) in CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MASPYGYYGYCQERHSAVFDLAGCGFEEEGYPVVDYESALQTAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .16758
                                                                                                                  .50550
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                                                                CDS
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57009. .57230
complement(join(73563. .73631,73893. .74134,74182. .74314))
/gene="P0493G01.13"
/note="hypothetical protein"
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/translation="MTVYRRGNVRTTPDQPSSGSDLERPCQNLGSTAITSVRTNCHARN
COMplement(join(73563..73631,73893...74134,74182...74314))
/gene="p0493601.13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="P0493G01.10"
join(67720. .67754,68296. .68374,68468. .68516,69708.
/gene="P0493G01.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAB39931.1"
/db_xref="GI:1346695"
/tzanslation="muyudodptwhtmevicaygmrsriwkeskfgmigyvkfvsctr
GEPKVFWTLSMSLVRGFRLPISCINRGRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains ESTs AU065507(C0785),AU081546(C0785)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GFPKVFWTLSMSLVRALGCLPHV'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains ESTs AU065507(C0785), AU081546(C0785)
unknown protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54115. .54318
/gene="P0493G01.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MSPVKVFGRAISINVSRVLVCLEEVGADYELVTVDFLAGEQNSP
EHVERNPFGKIPALQDGDLVLFESRAIAKYILRKYKSSKVDLLRESDIREAALVDVWT
EVEAHQYYPALSPIVFECIIFPIMRGVPTNQQVVHESLEKLKKVLETYEARLSGSRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative glutathione transferase"
/protein_id="BAB39929.1"
/db_xref="GI:13486693"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(52409. .52866,53006. .53054,53155./gene="P0493G01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(52409.
/gene="P0493G01.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo
49182. .
                                                                                                                                                                                                                                                                                                                                               join(67720. .67754,68296. .68374,68468.

/gene="p0493G01.11"

join(72007. .72166,72353. .72432,72937.

/gene="p0493G01.12"

join(72007. .72166,72353. .72432,72937.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="probably inactive due to stop codon(s) in CDS
pseudogene, glutathione transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probably inactive due to stop codon(s) in CDS
pseudogene, similar to non-LTR retroelement reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63015.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="BAB39930.1"
/db_xref="GI:13486694"
/translation="MHVVDGDSIWHTMEVLCAYGMQSRIWKDTKFDMIGYVKFVSCTR
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/note="probably inactive due to frameshift(s) in CDS
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                                                                                                                                                                                                                                                                                           /note="hypothetical protein"
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Direct Submission
Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington Submitted (15-NOV-2001) Genome Sequencing Center, Washington C
                                                                                                                                                                                                                                                                University School of Medicine, MO 63108, USA 5 (bases 1 to 72045)
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4 (bases 1 to 72045)
Waterston, R.H.
   Direct Submission Submitted (10-JAN-2002) Department of Genetics, Washington
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                                                                                                                                            Submitted (03-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                 Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (29-JUN-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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The sequence of Homo sapiens BAC clone RP11-811J9
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Sulston, J.E. and Waterston, R.
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AC092214
                                                            Waterston, R.
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/gene="P0493G01.15"
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/db_xref="G1:13466697"
/db_xref="G1:13466697"
/translation="M15APTTSAPAATRAARTAQARRRTTARGREORTPTDRGRRGELT
/translation="M15APTTSAPAATRAARTAQARRRTTARGREORTPTDRGRRGELT
GRSGGGDRVDGGDGAPAVFGGGEGADEDGDDLAIPMVATATDDGGCNGGAARLNRRQR
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/gene="p0493601.14"
/note="contains ESTS C72648(E2001),C71850(E0464)
unknown protein"
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/note="3' LTR"
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/protein_id="BAB39934.1"
/db_xrefr="G1:13486698"
/translation="MVGCEHMVLRVVLMTIKDRFTSFGCETLTVPTTSQRGQRLYLLY
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complement/7600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The clone sequenced to the left is RP11-563K23; the clone sequenced to the right is RP11-998A10, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-811J9; actual end is at base position 140619 of RP11-298A10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 15, 2001 this sequence version replaced gi:15625026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymorphisms have been identified between AC073264 and AC092214 
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence derived from pcr, base position 6122 to 6452 and 7046 to 7087.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAPPING INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was finished as follows unless otherwise noted:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restriction digest.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://bacpac.med.buffalo.edu)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://genome.wustl.edu/gsc
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                                                               /note="CpG_island (%GC=73.4, o/e=0.90, #CpGs=130)" 357. .360
/note="match to EST BE733203 (NID:g10147195)" 444...573
                                                                                                                                     /note="match to EST AI066553 (NID:g3367255) oo14g02.x1" 125. .1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="7"
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                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI-11"
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939. .1143
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                                                                  /note="similar to Mus musculus EST BB619995
                                                                                                                              note="match to EST AL556892 (NID:g12899973)"
                                                                                                                                                                                                                                                                                                                                                                      /note="match to EST AL545268 (NID:g12877749)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="match to EST AA292501 (NID:g1940488) zt30b03.r1"
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                                                                                                                                                                                                                                                                       (NID:g11616033)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 122,717 genomic DNA of 11g12
Published Only in DataBase (2000) In press
2 (bases 1 to 12271)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                          On May 30, 2000 this sequence version replaced gi:7023957
                                                                                                                                                                                                                                                                                                                                                                                                                URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-FEB-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 11 clone CMB9-83A3 map 11q12, WORKING DRAFT AP001186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 122717)
                     Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of Assembly program: Phrap; version 0.990329 Consensus quality: 114906 bases at least Q40 Consensus quality: 11892 bases at least Q30 Consensus quality: 120476 bases at least Q30 Insert size: 121517; sum-of-contigs
                                                                                                                                                                                                                                            Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
Project Information
                                                                                                                                                                                                       Center project name: HumDraftll Center clone name: CMB9-83A3
Quality coverage: 6.05x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                    Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                         Center: RIKEN Genomic Sciences Center(GSC)
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sapiens DNA, clone:CMB9-83A3.
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947. .1143
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(NID:g14498907)"
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(NID:g15570185)"
1020. .1143
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1001. .1143
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                                                                                                                                                                                                                                                                                                                                                                 Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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49520 63383: contig of 13864 bp in length
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49520..63383
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                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="11"
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/note="assembly_fragment"
75237. .84053
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63484. .75136
                                                                                                                                                                                              note="assembly_fragment"
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92774: contig of 8621 bp in length
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f 4258 bp in length
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f 3000 bp in length
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

July 31, 2002, 12:20:34; Search time 165.21 Seconds (without alignments)

1111e:
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1121 US-09-899-718A-3
1222 Million cell updates/sec
123 Sequence:
124 Sequence:
125 Secoring table:
126 JUNITITY_NUC
126 Gapop 10.0, Gapext 1.0
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Total number of hits satisfying chosen parameters:
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

383533 seqs, 122816752 residues

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4
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US-08-035-392-1	US-09-022-699-3	US-08-463-772-32	US-08-246-361A-32	US-08-464-517-32	PCT-US93-05000-32	US-08-939-727-15	US-08-939-727-2	US-08-442-281-15	US-08-442-281-2	US-08-442-282-15	US-08-442-282-2	us-07-757-390-15	US-07-757-390-2	US-09-018-635-22	US-09-176-657-5	US-09-210-168-1	US-08-939-727-16
Sequence 1, Appli	Sequence 3, Appli	Sequence 32, Appl	Sequence 32, Appl		Sequence 32, Appl		Sequence 2, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 15, Appl	Sequence 2, Appli	Sequence 22, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 16, Appl

## ALIGNMENTS

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                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: WA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THE INHIBITORS NUMBER OF SEQUENCES: 8
                                                  MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: IL 1 FILING DATE: 12-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/476,862 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                       LENGTH:
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                90..1472
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RESULT 3
US-09-078-294-7/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6225054
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 7, Application US/09078294 Patent No. 6265211
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Best Local S
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APPLICANT: Cancilla, Michael R.
TITLE OF INVENTION: A NOVEL NUCLEIC ACID MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/078,294
CURRENT FILING DATE: 1998-05-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: Davies Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Choo, Kong-Hong Andy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3250 AGAAACAAACAAACAAACAAA 3230
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            NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                          APPLICATION NUMBER: US/08/991,789A FILING DATE: 11-Dec-1997
                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                  STATE: Washington
                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                          CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 701 Fifth Avenue, Suite 6300
TELEFAX: (206) 682-6031
                                                                                                                                           CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
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road, Steven G.
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100.0%; Pred. No. 11;
tive 0; Mismatches
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RESULT 6
US-08-991-789A-169/c
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Best Local !
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Best Local Similarity
Matches 20; Conserv
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APPLICANT: Frudakis, Tony t
APPLICANT: smith, John M.
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: PSM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Mak1, David J.
REGISTRATION UNMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 AGAAACAAACAAACAA 167
                                                                148 AGAAACAAACAAACAA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/062,451 FILING DATE: 04-APR-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                          (206) 682-6031
(207) TD NO: 191:
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                                                                                                                               Conservative
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                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                          (206) 622-4900
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100.0%; Pr
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                                                                                                                                           95.2%; Score 20;
100.0%; Pred. No.
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Pred. No.
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Patent No. 6225054
GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                       Sequence 169, Application US/09062451 Patent No. 6344550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Fridakis, Tony l
APPLICANT: smith, John M.
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 169: SEQUENCE CHARACTERISTICS:
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                   NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                        STREET: 6300 CONTY: Seattle STATE: Washing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   840 AGAAACAAACAAACAA 821
                                                                                                COUNTRY:
                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 agaaacaaacaaacaa 20
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1265 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 701 Fifth Avenue, Suite 6300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                        Washington
                                                                                                                                                                 6300 Columbia Center, 701 Fifth Avenue
                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                Frudakis, Tony N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                      SEED and BERRY LLP
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US-08-991-789A-290
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INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                         INFORMATION FOR SEQ ID NO: 290:
SEQUENCE CHARACTERISTICS:
LENGTH: 1646 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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STRANDEDNESS: sing.
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
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                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: <UNKnown>
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND DIAGNOSIS OF BREAST CANCER
                    SEQUENCE DESCRIPTION: SEQ ID NO: 290:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                   NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Seed IP Law Group STREET: 701 Fifth Avenue, Suite 6300
                                     STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 98104-7092
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100.0%; Pred. No.
tive 0; Mismatcl
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Best Local Similarity
Matches 20; Conserva
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US-08-967-101-86
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                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                 GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1213 AGAAACAAACAAACAAACAA 1194
                  APPLICANT: ST. GEORGE-HYSLOP, APPLICANT: ROMMENS, JOHANNA M APPLICANT: FRASER, PAUL E TITLE OF INVENTION: GENETIC SETIILE OF INVENTION: TO ALZHEIM
                                                                                                                                                                                                                 1213 AGAAACAAACAAACAA 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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     NUMBER OF SEQUENCES:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                Application US/08967101
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100.0%; Pre
GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE 183
                                                                                                                                                                                                                                                                                           95.2%; Score 20;
100.0%; Pred. No.
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Best Local Similarity
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APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 86:
                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                 ATTORNEY/AGENT INFORMATION: NAME: Pitcher, Edmund R.
NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                               STREET: High
CITY: Boston
STATE: Massac
                                                       CLASSIFICATION:
                                                                       FILING DATE:
                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                          ZIP: 02110
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CITY: Boston
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EDNESS: single
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High Street Tower - 125 High Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          500 base pairs
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95.2%; Pred. No. 38;
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                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                             TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                          NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
70 ACAAACAAACAAACAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/124,698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
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                1 agaaacaaacaaacaaacaaa 21
                                                                          Local Similarity
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(617) 248-7100
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                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                       92.4%;
95.2%;
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Pred. No. 3
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Pred. No. 3
                                                          Mismatches
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                                                                           38;
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                                                                                     Length 500;
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RESULT 14
US-08-496-841C-86
US-08-496-841C-86
; Sequence 86, Application Us,...
; Patent No. 6210919
; Patent INFORMATION:
GENERAL INFORMATION:
ROMMENS, JOHANNA M
FRASER, PAUL E
FRASER, PAUL E
FRASER, PAUL SEQUENCES P
                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic) US-09-127-480-86
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES
TITLE OF INVENTION: TO ALZHEIMER'S DIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Pitcher, Edmund R. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/127,480 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                      1 agaaacaaacaaacaaa 21
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
                                                                                                                         TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED TO ALZHEIMER'S DISEASE
                                                                                                                                                                                                                                                                                                                                      ACAAACAAACAAACAAA 90
                                                                                                                                                                                                                                                                                                                                                                                                         20;
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STATE: New York COUNTRY: U.S.A.
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                                      CITY: New York
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High Street Tower - 125 High
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(617) 248-7100
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95.2%;
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Pred. No. 38;
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US-09-328-111-120/c
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; LOCATION: (1)...(504)
; OTHER INFORMATION: n = A,T,C
US-09-328-111-120
                                                                                                                                                           NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 120, Application US/09328111 Patent No. 6262333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                  APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUWAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT FILLING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bushnell, Steven E
APPLICANT: Carroll III, Eddie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Steinmann, Kathleen E. APPLICANT: Astle, Jon H.
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ford, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Catino, APPLICANT: Derti,
                                                reature:
NAME/KEY: misc_feature
                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                            LENGTH: 504
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CLASSIFICATION: <UDKnown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehlner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Burgess, Christopher
Bushnell, Steven E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endege, Wilson O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catino, Theodore J.
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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95.2%; Pred. No. 38;
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Search completed: July 31, 2002, 12:20:35 Job time: 11658 sec

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	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
OM nucleic - nuc	nucleic search, using sw model
Run on:	July 31, 2002, 12:11:53 ; Search time 5855.71 Seconds (without alignments) 48.403 Million cell updates/sec
Title:	US-09-899-718A-3
Sequence:	1 agaaacaaacaaacaaa 21
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	13736207 segs, 6748477542 residues
Total number of	Total number of hits satisfying chosen parameters: 27472414
Minimum DB seq l Maximum DB seq l	seq length: 0 seq length: 2000000000
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	EST:* 1: em_estba:* 2: em_esthum:* 3: em_estin:*
	5: em_escunu:* 6: em_estov:*
	9: gD_esti:* 10: gb_esti:* 11: ab htc:*
	12: gb_gss:* 13: em_gss_inv:* 14: em_gss_inv:* 15: em_gss_inv:* 16: em_gss_v:+:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AI792899	AI251238	BB072882	AI733998	AA457363	AA719825	AI733948	AI253971	BH105347	AZ493323	AA639520	BF922085	AI345073	BI043282	BG998551	вJ046075	AZ504073	ID			SUMMARIES
	AI251238 qv55q05.x	BB072882 BB072882	AI733998 qv55g05.x	AA457363 aa91f12.r	AA719825 zh39d02.s	AI733948 qv54a05.x	AI253971 qv54a05.x	BH105347 RPCI-24-3	AZ493323 1M0327M24	AA639520 nq91a09.s	BF922085 CM2-NT017	AI345073 tb62b07.x	BI043282 PM4-OT020	BG998551 PM4-HT130	вJ046075 вJ046075	AZ504073 1M0344C07	Description			

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100.0	100.0			100.0		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
270 275 275	267	262	260	257	256	255	251	249	247	245	243	241	239	231	228	227	224	223	222	202	201	196	194	190
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AZ413748 AZ772597 BB482086	AQ675744	BB425056	AZ597098	T73967	AV264285	AZ414740	AV336252	BE852501	AV230114	AV262627	AV281580	AZ221788	BF747295	AV229441	BB183787	AV317088	BE071169	BB536522	BB150403	AI465751	AA839213	AI792857	AI549855	AZ656418
AZ772597 1M0593B07 BB482086 BB482086	BE850705 uw21d04.y AQ675744 HS_5489_B	B	AZ597098 1M0410E17	~	AV264285 AV264285	AZ414740 1M0189117	AV336252 AV336252	BE852501 uw21d04.x	AV230114 AV230114	AV262627 AV262627	$\rightarrow$	AZ221788 RPCI-23-4	BF747295 RC1-BT025	AV229441 AV229441	вв183787 вв183787		BE071169 RC3-BT050	вв536522 вв536522	BB150403 BB150403	AI465751 vw95a09.y	AA839213 vw95a09.r	AI792857 qv54a05.y	AI549855 Vw95a09.x	AZ656418 1M0531M23

# ALIGNMENTS

FEATURES SOURCE	JOURNAL COMMENT	AUTHORS TITLE	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AZ504073/c LOCUS DEFINITION
<del></del>	Unpublished (2000) Contact: Robert B. Weiss University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT RA112, USA	Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.  Mouse whole genome scaffolding with paired end reads from 10kb	AZ504073.1 GI:10685389 GSS. house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.	AZ504073 58 bp DNA linear GSS 05-OCT-2000 LM0344CO7F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0344CO7 F, DNA sequence.

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in X. laevis embryo
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1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      African clawed frog.
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a 9 c 10 g 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector PNDA STATE PROPERTY OF THE PROPERTY OF THE PROPERTY OF PROPERTY OF PROPERTY OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The
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                                                                                                                                                                                                                              /tissue_type="whole embryo"
/dev_stage="stage 15"
                                                                                                                                                                                                                                                                                                                                library"
                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:8355"
/clone="xL006d02"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="NIBB Mochii normalized Xenopus neurula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Xenopus laevis"
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Pred. No. 9.6e+04;
Score 21;
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FEATURES

BI043282 RESULT COMMENT

TITLE

SOURCE VERSION

KEYWORDS

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14 AGAAACAAACAAACAAACAAA 34
                                                                                                                   Local Similarity
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                                          1 agaaacaaacaaacaaa 21
                                                                                               21;
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Seq primer: puc 18 forward
High quality sequence stop: 139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 139)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                         54 a
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                               /note-"Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-1lbrary was made by clonking products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone_lib="HT1301"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                 100.0%; Score 21; DB 10; 100.0%; Pred. No. 6.2e+04;
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                                                      Homo sapiens
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                     EST
                                                                                                                     AI345073.1 GI:4082279
                                                                                                                                              AI34507
                                                                                                                                                             mRNA sequence
                                                                                                                                                                                                             AI345073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-OT0201-
120301-001-d03_1&t3=2001-03-12&t4=1)
Seq.primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Simpson A.J.G.
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Ludwig Institute for Cancer Research
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/db_xref="taxon:9606"
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                                                   Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                            Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F. F., Goldman, G., H., Carvalho, A. F., Matsukuma, A., Baid, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Dias Neto, E., Garci
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                                                                                                                                                                                                                                   Simpson,A.J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40UP from Gibco.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
+55-11-2704922
+55-11-2707001
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                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
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Directionally cloned. Size-selected on agarose
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/clone_lib="NCI_CGAP_Brn20"
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/dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html
seg primer: -40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 150)
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/db_xref="taxon:9606"
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/note="Organ: colon; Vector: p7773D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from RER+ colon tumor, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco
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                                                                                                        /tissue_type="colon tumor RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                    /clone="IMAGE:1159672"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 156)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 10000
Plate: 0327 row: M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
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and Wright,D.,Weiss,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gi|4732114|gb|AF129072.1), a copy-number
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                                                                                                                                                                                                                                                                               musculus C57BL/6J (male) was obtained from the Jackson
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                                                                                                                                                                                                                                                                                                                                                       /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Mouse 10kb plasmid UUGC1M library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-24. For BAC

Library availability, please contact Pieter de Jong

(pdejong@mail.cho.org). Clones may be purchased from BACPAC

Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC @page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Other_GSSs: RPCI-24-379D17.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levin Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E. Russell, D., de Jong, P. and Fraser, C.M. Mouse BAC End Sequences from Library RPCI-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RPCI-24-379D17.TJ RPCI-24 Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH105347.1 GI:14934204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 156)
                                                                                                            94
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                                                                                                                                                        /Cell_type="Spleen/Brain"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-74 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                             BamHl sites using MboI
                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-379D17"
/clone_lib="RPCI-24"
                                                                                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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Pred. No. 5.8e+04;
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                                                                                                                                           partially digested male C57BL/6J
                   DB 12;
  .8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                 Length 156;
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs -r@mail.nih.gov

Tissue procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llni.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
                                         Homo sapiens
                                                                                EST
   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                               qv54a05.x5 NCI_CGAP_Ov32 Homo
                                                                                                                                                                     AI733948
                                                                                             AI733948.1
                                                                                                                                 mRNA sequence.
                                                              numan
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qv54a05.x1 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985360 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "

23 c 31 g 34 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1985360"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="NCI_CGAP_Ov32"
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Pred. No. 5.6e+04;
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                               bp mRNA linear EST 14-JUN-1999
sapiens cDNA clone IMAGE:1985360 3',
                                                                                                                                                                  mRNA
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National Cancer Institute / National Institute of Dental Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA719825 177 bp mRNA linear EST 30-DEC-1997
zh39d02.sl Soares_pineal_gland_N3HPG Homo sapiens cDNA clone
IMAGE:414435 3' similar to contains Alu repetitive element; contains
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                          Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
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                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          element LTR1 repetitive element ;, mRNA sequence.
                                                                                                         Contact: Wilson RK
                                                                                                                                  Unpublished (1997
                                                                                                                                                             white,Y., Wylie,T., Waterst
washU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.
Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library.

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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. ET from Amersham
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aa91f12.rl Stratagene fetal retina 937202 Homo sapiens cDNA clone
IMAGE:838703 5' similar to contains element MER22 repetitive
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev1 ET from Amersham
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//lab_host="DH10B (ampicillin resistant)"
/note="Organ: pineal gland; vector: pT7T3D (Pharmacia)
/note="Organ: pineal gland; vector: pT7T3D (Pharmacia)
/note "Organ: pineal gland; vector: pT7T3D (Pharmacia)
/with a modified polylinker; Site_1: Not I: Site_2: Eco RI;
/strand cDNA was primed with a Not I - oligo(dT) primer
/st strand cDNA was primed with a Not I - oligo(dT) primer
/st strand cDNA was primed with a Not I and cloned
RI adapters (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of a modified pT7T3 vector
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/db_xref="GDB:1319706"
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/lab_host="SOLR (kanamycin resistant)"
                                                      /clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
                                                                                                                                                /clone="IMAGE:838703"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original clone citation: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tissue Procurement: W. Marston Linehan, M.D., Rodrigo F. Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: The I.M.A.G.E. Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qv55g05.x5 NCI_CGAP_Ov32 Homo sapiens cDNA clone IMAGE:1985528 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This read is a RESEQUENCE of a previously sequenced human clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI733998.1 GI:5055111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 orientation)
Length: 238
                                                                                                                                  /note="Organ: ovary; Vector: pAMP1; mRNA made from ovarian carcinoma, cDNA made by oligo-dT priming.

Non-directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Non-amplified library. "

32 c 34 g 37 t
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                                                                                                                                                                                                                                                    /tissue_type="papillary serous carcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:1985528"
/clone_lib="NCI_CGAP_Ov32"
                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                       ∕organism="Homo sapiens"
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Pred. No. 5.4e+04;
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Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata
Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y.,
Suzuki, H., Szzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya
, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I.,
Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino
M., Muramatsu, M. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             trehalose and its application for the synthesis of full length CDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,p. Nishiyama,y., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory
                                                                                                   /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                     /lab_host="DH10B"
                                                                                                                                                                                                                                               /sex="male"
                                                                                                                                                                                                                                                             /clone_lib="RIKEN full-length enriched, adult male colon"
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/clone="9030619B06"
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/strain="C57BL/6J"
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BASE COUNT ORIGIN Query Match 100.0%; Score 21; DB 9; Length 184; Best Local Similarity 100.0%; Pred. No. 5.3e+04; Matches 21; Conservative 0; Mismatches 0; Indels 

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Search completed: July 31, 2002, 12:11:57 Job time: 13470 sec

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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7: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001A.DAT: *
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd.
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AAC13041
AAV87203
AAC44102
AAS46192
AAD09952
ABD16382
                                     AAC79000
                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Human drug metabol
Human nervous syst
Human secreted pro
p75 Tumour Necrosi
                                                                                                                                                                                                                                             Description
                                                                                                                     Human secreted pro
EST clone BN40. H
Arabidopsis thalia
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22	3 K	22	22	22	22	22	22	22	22	20	22	22	22	22	24	22	22	23	22	22	22	22	23	21	21	22	22	12	22	22	22	22	20	12	
AAK89370	AAK81266	AAL06122	AAS26724	AAI67272	AAI67271	AAK81010	AAK70316	AAK70315	AAK70314	AAV83943	AAK89493	AAK74469	AAK89492	AAK74467	ABI99827	AAL04707	AAK51993	AAS84690	AA160242	AAK53345	AAI58456	AAK52361	ABL26224	AAH51796	AAA49207	AAH15452	AAC83951	AAQ10907	AAK85886	AAK85885	AAK85884	AAH48860	7	AAQ10956	
Human immune/haema Human digestive sy										н		Human immune/haema		immine/ha		reproductiv	Human polynucleoti	_			Human polynicleoti	Human polynucleoti	Drosophila melanog	Chromosome 13d31-d			Human 40 kDa TNF i	-3					THOUSE F	Encodes human 75kD	

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### ALIGNMENTS

ΡΙ	XX A	PR	X PF	XX D	ΧΧ	XFT	H H	ΞH	SO 44	×	X	KW	XX	X	X	AC	×	3	RESULT
Quadrifoglio F, Scaggiante B;	(SAIC-) SAICOM SRL.	04-DEC-1995; 95IT-OMI2539.	04-DEC-1996; 96WO-EP05388.	12-JUN-1997.	W09720924-A1.	/*tag= a /note= "phosphodiester oligonucleotide"	modified_base 135		Synthetic.	Lymphoblastic tumour; ss.	tumoural cell line; cytotoxic activity; tumour cell; lymphoma;	Phosphodiester; selective binding; cell viability; growth;	Phosphodiester oligonucleotide 29 with cytotoxic activity.	24-FEB-1998 (first entry)		AAT93839;		830 standard. DNA. 35	RESULT 1

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AAQ89544

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RESULT
AAC13041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The oligonucleotides (see also AAT93811-27) are believed to selectively bind and sequester some proteins which are essential to the viability and srowth of tumoural cell lines. They have specific and selective cytotoxic activity against tumour cells, and can be used for treating tumours of the liquid type, in particular of lymphoblastic origin, and of the solid type, in particular lymphomas. Oligonucleotides AAT93834-36 were created to determine the relevance of the specific features of the above generic formula, in determining cytotoxic activity. The present sequence is different from the generic sequence in that the sequence has flanking fragments containing C and T bases. The results showed that sequences having flanking fragments containing C and T bases do not exert any significant cytotoxic activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel phosphodiesteric oligonucleotides AAT93837-41 are based on the generic formula, in the 3'-5' or 5'-3' direction:

(GaTa')a''-(GbTb')b''-(GcTc')c''-(GdTd')d''-(GeTe')e''-(GfTf')f''-

(G-Tg')g''.N', where:

N and N' = T or G, equal or different from each other;

x = 0-8, equal or different from each other;

a', b', c', d', e', f', and g' = 0-10, equal or different from each other;

a', b', c', d', e', f', and g' = 0-30, equal or different from each other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New phospho:di:esteric oligo:nucleotide(s) - which exert a specific and selective cytotoxic effect on tumour cells, for treating both solld and liquid tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 12; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-319771/29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            each other;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAC13041 standard; cDNA; 140 BP
                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                               Human secreted protein 5' EST, SEQ ID NO: 17116.
                                                                                                                                                                                                                                                                                                                                                 06-OCT-2000
WPI; 2000-500381/45
                                Dumas Milne Edwards J,
                                                              (GEST ) GENSET
                                                                                                                               21-FEB-2000; 2000EP-0200610
                                                                                                                                                                06-SEP-2000
                                                                                                                                                                                                EP1033401-A2
                                                                                                                                                                                                                                 Homo
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                                                                                                                                                                                                                               sapiens
                                                                                                                                                                                                                                                              therapy;
                                                                                                                                                                                                                                                                                 5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 0 A; 4 C; 5 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                              chromosome mapping; ss
                                                                                                  99US-0122487
                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                    Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                     Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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RESULT
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively todentified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and ascretion ventore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 140 BP; 47 A; 38 C; 38 G; 17 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              Expressed sequence tag; secreted protein; haematopoiesis regulator; tissue growth; activin; inhibin; tumour invasion suppressor; EST; h chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                WO9845435-A2
                                                                                                                                                                                                                                                                                                                                                                                                               receptor; ligand; anti-inflammatory; tumour inhibitor; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAV87203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV87203 standard; cDNA; 384
                                                                                                                                                                                                                                                10-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 agaaacaaacaaacaaacaaa 129
                                                                                                                               WPI; 1999-070076/06.
                                                                                                                                                                                 Agostino MJ,
                                                                                                                                                                                                                                                                                10-APR-1998;
                                                                                                                                                                                                                                                                                                                 15-OCT-1998
                                                                            New polynucleotides encoding human secreted proteins - derived from e.g. human blood, kidney, feetal lung, placenta, testes, brain,
                                                                                                                                                                Racie
                                                                                                                                                                                                               (GEMY ) GENETICS INST INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID 17116; 71pp + CD-ROM; English.
                                                                                                                                                              J, Jacobs K,
Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                 97US-0835913.
                                                                                                                                                                                                                                                                                    98WO-US06954.
                                                                 retina and colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                  Lavallie ER, Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 21;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                   cDNA libraries
                                                                                                                                                                                     мссоу ЈМ,
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0;

This sequence represents an expressed sequence tag (EST), and is

Claim 1;

Page 487; 633pp; English.

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AAC44102
XX
AC4
XX
AC AAC4
XX
AC AAC4
XX
ATA
DT 18-C
XX
DT 18-C
XX
W Hybr
KW Hybr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotide of the invention. The polynucleotides of the invention are all secreted EST sequences isolated from a variety of human tissue sources. The EST sequences and proteins encoded by them are predicted to have useful biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, tumour inhibition activity. The EST sequences are also stated to be useful for gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana DNA fragment SEQ ID NO: 41638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC44102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000EP-0301439.
             99US-0121825

99US-0123548

99US-0125788

99US-0126785

99US-0126785

99US-0128714

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99US-013047

99US-013044

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99US-013248

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99US-01342163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G; 123
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15-JUL-1999;
16-JUL-1999;
16-JUL-1999;
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14-JUN-1999;
16-JUN-1999;
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17-JUN-1999;
990S-0135353
990S-013629
990S-0136021
990S-0136021
990S-0137528
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99US-0134370.
99US-0134768.
99US-0134941.
99US-0135124.
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99US-0145913. 99US-0145918. 99US-0145919. 99US-0145951. 99US-0146386.

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25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
01-MAR-2000;
02-MAR-2000;
03-MAR-2000;
14-MAR-2000;
14-MAR-2000;
15-MAR-2000;
21-MAR-2000;
11-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; col adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disord PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS46192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNA encoding PRO polypeptide sequence #268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001 (first entry)
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Local
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Similarity 100.0%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 1106
   2000WO-US05601
2000WO-US05841
2000WS-H97202P
2000US-H89320P
2000US-H9932P
2000US-H9932BP
2000US-191007P
2000US-191048P
2000US-191048P
2000US-193032P
2000US-193032P
2000US-193032P
2000US-193032P
2000US-194449P
2000US-194447P
2000US-196447P
2000US-19650P
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2000US-19650P
2000US-19652P
2000US-19655P
2000US-199550P
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99US-0161106.
99US-0161359.
99US-0161361.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
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Pred. No. 1.2e+02;
); Mismatches 0;
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27-JUL-1999;
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02-AUG-1999;
02-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
06-AUG-1999;
10-AUG-1999;
11-AUG-1999;
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99US-0147204
99US-0147204
99US-0147302
99US-0147152
99US-0147433
99US-0147433
99US-0148319
99US-0148341
99US-0148565
99US-0149426
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99US-0149929
99US-0149929
99US-0150566
99US-0150566
99US-0151065
99US-0151065
99US-0151065
99US-0151233
99US-0151233
99US-015438
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99US-0155438
99US-0155458
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99US-0155458
99US-0155466
99US-0159330
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99US-0159588
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                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                  Human; drug metabolising enzyme; DME-17; immunosuppressive; gene therapy; cytostatic; autoimmune disorder; inflammatory disorder; atherosclerosis; esteoporosis; eye disorder; hepatic tumour; Addison's disease; cretinism; rheumatoid arthritis; acquired immune deficiency syndrome; AIDS; anaemia; developmental disorder; endocrine disorder; iritis; acromegaly; epilepsy; thyrotoxicosis; pancreatic disorder; diabetes mellitus; obesity; adenoma; gastrointestinal disorder; nodular hyperplasia; conjunctivitis; glaucoma;
                            actinic keratosis;
                                                                                                                                                                              Human drug metabolising enzyme (DME-17) cDNA.
                                                                                                                                                                                                                  12-SEP-2001 (first entry)
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02-JUN-2000;
05-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1106 BP; 325 A; 226 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 535; 774pp; English.
                                                                                                                                                                                                                                                                                                                                                                           845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-AUG-2000;
08-NOV-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Smith V, W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000WO-US14941.
2000WO-US15264.
2000WS-209832P.
2000WO-US20710.
2000WS-0644848.
2000WO-US23328.
2000WO-US33678.
2000WO-US33678.
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                       metabolic disorder; dysphagia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Desnoyers L, Goddard A, Godowski pJ,
atanabe CK, Wood WI, Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21; DB 22;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1106;
                         anorexia;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                           Matches
                                                                           Query Match
Best Local
                                                                                                                                                                    disorder such as actinic keratosis, atherosclerosis; developmental disorder such as epilepsy, anaemia; endocrine disorder such as acromegaly, cretinism, thyrotoxicosis; pancreatic disorder such as diabetes mellitus; eye disorder such as conjunctivitis, glaucoma, iritis metabolic disorder such as Addison's disease, obesity; gastrointestinal disorder such as anorexia, dysphagia and hepatic tumours including nodular hyperplasia, adenomas and carcinomas. DME DNA is useful for creating 'knockin' humanised animals (pigs) or transgenic animals (mice or ratts) to model human disease. DME DNA is also in useful is gene therapy. DME and its immunogenic fragments are useful for screening
                                                                                                                                                                                                                                                                                                                   The present sequence is human drug metabolising enzyme (DME-17) cDNA. Human DME and its nucleic acid molecule are useful for the diagnosis, treatment and prevention of disorders associated with increased or decreased expression of DME. Examples of such disorders include, autoimmune/inflammatory disorder such as acquired immune deficiency syndrome (AIDS), rheumatoid arthritis, osteoporosis; cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drug metabolizing enzymes and encoding polynucleotides, useful for diagnosing, treating and/or preventing autoimmune, inflammatory, coproliferative, developmental, endocrine, eye, metabolic, and
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Ring HZ,
                                                                                                                               Sequence 1122 BP; 338 A; 228 C; 261 G;
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    845
                                                                                                                                                                 libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gastrointestinal disorders -
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21-JAN-2000; 2000US-0177443;
28-JAN-2000; 2000US-0178574,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE GENOMICS INC
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                                                        Similarity 100
21; Conservative
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, Hillman JL,
DB, Tang YT,
                                                                                                                                                         of compounds in several drug screening assays.
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213..752
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123..212
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123..755
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YT, Lal P,
                                                                      100.0%;
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865
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                                                          0;
                                                                 Score 21; DB 22;
Pred. No. 1.1e+02;
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                                                        Mismatches
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                                                                                                                                295
                                                                                                                               T; 0 other;
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                                                                                   Length 1122;
                                                     Indels
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                                                     0;
                                                     Gaps
                                                     0,
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ABA16382,

ABA16382 standard; DNA; 1409 BP

ABA16382

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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
26-JUL-2000;
26-JUL-2000;
14-AUG-2000)
14-AUG-2000;
12-AUG-2000;
12-AUG-2000;
13-AUG-2000;
14-AUG-2000;
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16-AUG-2000;
17-AUG-2000;
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19-AUG-2000;
19-AUG-2000;
19-AUG-2000;
10-SEP-2000;
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2000US-0184664.

2000US-0184664.

2000US-0186350.

2000US-0198074.

2000US-0198123.

2000US-0209467.

2000US-020467.

2000US-0214886.

2000US-0216847.

2000US-0216847.

2000US-0216848.

2000US-0216880.

2000US-0217488.

2000US-0217488.

2000US-0218890.

2000US-0218290.

2000US-0218296.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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                                                                                                                                                                                                                                                                                                                                                                      2000US-0225268.
2000US-0225270.
2000US-0225447.
2000US-0225757.
2000US-0225757.
2000US-0225759.
2000US-0225759.
2000US-0227182
2000US-0227009
2000US-02292874
2000US-0229343
2000US-0229344
2000US-0229344
2000US-0229346
2000US-0229345
2000US-0229509
2000US-0239438
2000US-0239438
2000US-0239438
2000US-0231243
2000US-0231244
2000US-0231244
2000US-0231244
2000US-023124
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            25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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21-SEP-2000;
25-SEP-2000;
           13-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
03-OCT-2000;
03-OCT-2000;
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2000US-0234274
2000US-0234997
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2000US-0237039.
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2000US-0246528.
2000US-0246532.
2000US-0246609.
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2000US-024617

2000US-0246475

2000US-0246476

2000US-0246476

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2000US-0246523

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2000US-0246523
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2000US-0241787.
2000US-0241808.
2000US-0241809.
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2000US-0239935.
2000US-0239937.
              2000US-0246610
2000US-0246613
2000US-0249207
2000US-0249207
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2000US-0249211
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2000US-0236370
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                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                               Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticorvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorden; neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                                                         AAC79000 standard; DNA; 1688 BP
                                                                                                                                               Human secreted protein gene 4 clone HCEGS49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1409 BP; 361 A; 334 C; 324 G; 390 T; 0 other;
           Homo sapiens
                                                                                                                                                                                          14-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 8713; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC
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                                                                                                                                                                                                                                                                                                                                                 676 AGAAACAAACAAACAAACAAA 656
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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2000US-0251988.
2000US-0256719.
2000US-0251479.
2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251999.
2000US-0251990.
2000US-0254097.
2001US-0254097.
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 22;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                      cardiovascular disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local S
                                                                               Homo sapiens
                                                                                                                                                        p75 Tumour Necrosis Factor Receptor.
                                                                                                                                                                                             31-OCT-1995 (first entry)
                                                                                                                                                                                                                                  AAQ89544;
                                                                                                                                                                                                                                                             AAQ89544 standard; DNA; 2224 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                              receptor; ss.
                                                                                                                         Ligand; tumour necrosis factor; nerve growth factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1688 BP; 516 A; 310 C; 384 G; 478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 317; 367pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in the prevention, treatment and diagnosis of cancer, disorders, cardiovascular disorders and neurological diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fourty nine nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-1999;
14-JAN-2000;
                                                                                                                                                                                                                                                                                                                                               875 agaaacaaacaaacaaacaaa 895
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          Location/Qualifiers 90..1475
/*tag= a
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Pred. No.
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0;

/product- p75 TNF receptor.

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FITTI
/transl_except= CCA misc_difference 1146..1148
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misc_difference 1149..1151
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misc_difference 1161..1163
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/transl_except= TCA encodes Histidine.
misc_difference 1194...1196
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misc_difference 2000..2002
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misc_difference 2003..2005
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1140..1142
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1155..1157
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1158..1160
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1152..1154
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1191..1193
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1188..1190
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1176..1178
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1173..1175
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1170..1172
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1182..1184
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1167..1169
                                                /transl_except=
2017..2018
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2015..2016
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2012..2014
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2006..2008
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                        /transl_except=
2019..2021
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         /transl_except= CAG
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                                                                                                                                                                                                                                                         AGC encodes Glycine
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                                                                                  CAT
                                                                                                          GGT encodes Proline
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                                                          GGG
                                 ACC
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                                                                                                                                                                                                                                                                                                                                                         encodes Serine
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                                                                                                                                  encodes Alanine
                                                                                                                                                                                  encodes Threonine
                                                                                  encodes Valine
         encodes
                                                          encodes Glutamic acid.
                                  encodes
                                                                                                                                                                                                                                                                                                          Serine
           Serine
                                  Alanine
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AAQ10956/c
ID AAQ109
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A ligand to a member of the tumour necrosis factor (TNF)/nerve growth factor (NGF) receptor family which binds either to the region of the 4th-Cys rich domain of the receptor, or to the region between it and the cell membrane may be used in the production of a pharmaceutical composition for increasing the inhibitory effect of a soluble receptor of the TNF/NGF receptor family. This sequence encodes the p75 TNF receptor. N in the sequence represents an unidentified nucleotide (poor reproduction in specification).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-OCT-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2224 BP; 432 A; 697 C; 688 G; 400 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Figure 2; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumour necrosis factor (TNF) receptor ligand - used to increase inhibitory effect of a soluble TNF receptor
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(WALL/) WALLACH D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1993;
                                           20-APR-1990;
12-SEP-1989;
08-MAR-1990;
                                                                                                                                                                                                                    autoimmune glomerulonephritis; lymphokine; cytokine.
                                                                                                                                                                                                                               Tumour Necrosis Factor; binding proteins; septic shock;
                                                                                                                                                                                                                                                       Encodes human 75kD TNF-binding protein.
                                                                                                                                                                                                                                                                              24-MAY-1991
                                                                                                                                                                                                                                                                                                     AAQ10956;
                                                                                                                                                                                                                                                                                                                          AAQ10956 standard;
Brockhaus M,
                                                                                          31-AUG-1990;
                                                                                                                 20-MAR-1991.
                                                                                                                                       EP417563-A.
                     (HOFF ) HOFFMANN-LA ROCHE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                               (first entry)
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 Dembic Z,
                                             90CH-0001347.
89CH-0003319.
90CH-0000746.
                                                                                           90EP-0116707
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                              /product= 75kD TNF-BP
                                                                                                                                                                                                                                                                                                                           DNA; 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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  Gentz R,
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Pred. No. 1.1e+02;
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  Lesslauer W,
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    Lotscher H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                               20-APR-1990;
12-SEP-1989;
08-MAR-1990;
Brockhaus M,
Schlaeger E;
                                                                                                                    31-AUG-1990;
                                                                                                                                                01-SEP-1999.
                                                                                                                                                                                                                                                                                                                 Tumour necrosis factor binding protein; TNF; insoluble protein; agonist; anti-inflammatory; antimalarial; treatment; septic shock; inflammation; autoimmune glomerulonephritis; cerebral malaria; immune response;
                                    (HOFF ) HOFFMANN LA ROCHE & CO AG F.
                                                                                                                                                                          EP939121-A2
                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Partial amino acid sequences were determined for the 55 and 75kD TNF-BPS (see AARI1072-R11081) and oligonucleotide primers were synthesised based on these partial sequences. The primers were used to produce a cDNA fragment for use as approbe to screen a human placental cDNA bank constructed in lambda gtll. Positive clones were identified and sequenced. Repeated sequencing showed a discrepancy at position 7 such that the third codon encodes either Thr or Ser. DNA constructs comprising the TNF-BP coding sequence may also contain a fragment encoding a human Ig domain. Recombinant constructs are used to transform cells to confer improved TNF-
                                                                                                                                                                                                                                                                                                           antagonist; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                     Human tumour necrosis factor binding protein cDNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ09171 standard; cDNA; 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2339 BP; 494 A; 720 C; 685 G; 439
                                                                                                                                                                                                                                                                                                                                                                                                      18-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Fig 1; 26pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insoluble tumour necrosis factor binding proteins - and DNA encoding them, useful in pharmaceutical prods. and for antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              See also AAQ10955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binding properties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-081851/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l agaaacaaacaaacaaa 21
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           Dembic Z,
                                                               90CH-0001347.
89CH-0003319.
90CH-0000746.
                                                                                                                  90EP-0116707
                                                                                                                                                                                               /"-ray" a
/product= "TNF binding protein"
/note= "Partial security"
                                                                                                                                                                                                                                          Location/Qualifiers
1..1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                           "Partial sequence, no start codon given"
                                                                                                                                                                                                                                                                                                            ds.
           Gentz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 1.1
0; Mismatches
         Lesslauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T; 1 other;
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        Loetscher
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Best Local Similarity
                                                                                          08-MAR-1990;
20-APR-1990;
31-AUG-1990;
31-AUG-1990;
WPI; 2001-559312/63
                        Brockhaus M,
Schlaeger E;
                                                                                                                                                  12-SEP-1989;
                                                                                                                                                                            31-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel homogeneous insoluble proteins (I), their (in)soluble fragments (Ia) and their salts that can bind tumour necrosis factor (TNF). The products of the invention have anti-inflammatory and antimalarial activity (I) and (Ia) are used (i) to treat diseases in which TNF is involved (e.g. septic shock, autoimmune glomerulonephritis, cerebral malaria, immune responses and inflammation), (ii) to purify TNF; (iii) to identify TNF (ant)sgonists and (iv) for diagnostic determination of TNF in body fluids. Antibodies raised against a tumour necrosis factor binding protein fragment described in the method of the invention.
                                                              (HOFF ) HOFFMANN LA ROCHE & CO AG
                                                                                                                                                                                                                                  EP1132471-A2
                                                                                                                                                                                                                                                                                                                                                         antiprotozoal; treatment; meningococcal sepsis; cerebral malaria; autoimmune glomerulonephritis; ds.
                                                                                                                                                                                                                                                                                                                                                                             TNF; tumor necrosis factor binding protein; TNFBD; treatment; insoluble protein; antiinflammatory; immunosuppressive; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                             Human TNFBP-associated DNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH48860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH48860 standard; DNA; 2339 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4a; Fig 4; 25pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New insoluble proteins, and fragments, that bind to tumor necrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor, used to treat e.g. septic shock or cerebral malaria
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                                                                                                                                                                                                                                                                                                                                 sapiens
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                                                                                                                                                                           2001EP-0108117.
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                                       Dembic
                                                                                                                   90CH-0000746.
90CH-0001347.
                                                                                         99EP-0100703
                                                                                                         90EP-0116707
                                                                                                                                                  89CH-0003319
                                                                                                                                                                                                                                                        /product= "TNFBP-associated protein"
                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                          /*tag=
                                    Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score
100.0%; Pred.
                                    Gentz R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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                                                                'T]
                                    Lesslauer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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DR XXX
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AAK85884/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes novel insoluble proteins (I), also their (in) soluble fragments and pharmaceutically acceptable salts, able to bind tumor necrosis factor (TNF) and in homogeneous form. The products of the invention have antiinflammatory, immunosuppressive, antibacterial, antiprotozal activity. (I), and related recombinant proteins, are used to treat diseases mediated by TNF, e.g. shock in cases of meningococcal sepsis; development of autoimmune glomerulonephritis and cerebral malaria. Also (I), or antibodies specific for them, are used for diagnostic determination of TNF in body fluids, for affinity purification of TNF and for identifying (ant)agonists of TNF. This sequence encodes a human TNF binding protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4a; Fig 4; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New homogeneous, insoluble proteins that bind tumor necrosis factor (TNF), useful for treating TNF-mediated disorders, e.g. inflammation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2339 BP; 494 A; 720 C; 685 G; 440 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40696.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAK85884 standard; DNA; 2357 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAK85884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                28-JUN-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                  16-MAR-2000;
17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 agaaacaaacaaacaaa 21
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                                                                                                                                                                                                                                                                                 2000US-0180628.
2000US-0184664.
2000US-0186350.
               2000US-0216647.

2000US-0216880.

2000US-0217487.

2000US-0217496.

2000US-0218290.

2000US-02218290.

2000US-0220964.

2000US-0224518.

2000US-0224518.
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2000US-0209467.
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        06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
12-SEP-2000;
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25-SEP-2000;

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06-CCT-2000;

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14-AUG-2000;
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01-SEP-2000;
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2000US-0226868.
2000US-0227182.
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2000US-0225266.
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2000US-0225268.
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2000US-0229287.
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2000US-0232399.
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17-NOV-2000;
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2000US-0249265
2000US-0249297
2000US-0249299
2000US-0249299
2000US-0249390
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2000US-0250391
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2000US-0249212.

2000US-0249214.

2000US-0249214.

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2000US-0249217.

2000US-0249217.

2000US-0249218.

2000US-0249245.
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2000US-0251990.
2000US-0254097.
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2000US-0251868.
2000US-0251869.
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2000US-0251988.
2000US-0256719.
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2000US-0246532.
2000US-0246601.
2000US-0246610.
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2000US-0246611.
2000US-0249207.
2000US-0249208.
2000US-0249208.
2000US-0249210.
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                                                                                                                                                                                                                   SCI INC
                                                                                                                                                                                                    Ruben SM;
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WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 40696; 3071pp + Sequence Listing; English

cc amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic cc activity, and can be used in gene therapy and vaccine production. (1) cc proteins and polynucleotides may be used in the prevention, diagnosis and ct treatment of diseases associated with inappropriate (1) expression. For cc example, they may be used to treat disorders associated with decreased cc expression by rectifying mutations or deletions in a patient's genome cc that affect the activity of (1) by expressing inactive proteins or to cc supplement the patients own production of (1). Additionally, (1) cc polynucleotides may be used to product the secreted (1), by inserting cc protein. (1) proteins and polynucleotides may be used to provent. (1) cancers and treat immune/haematopoietic-related diseases, especially cc ancers and cancer metastases of haematopoietic-derived cells. AAK64703 cc sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention. AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

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AAK85885/
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14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
22-AUG-2000;
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14-AUG-2000;
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07-JUL-2000;
11-JUL-2000;
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30-JUN-2000;
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17-MAR-2000;
18-APR-2000;
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14-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                      31-JAN-2000;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2357 BP; 677 A; 465 C;
                                                                                                                                                                                                                                                                                                              19-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                  17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; gene therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40697
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2000US-0229287.
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2000US-0225214

2000US-0225266

2000US-02525214

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2000US-025526

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2000US-0184664.
2000US-0186350.
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11-SEP-2000

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2000US-0231242.
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AAK85886;

07-NOV-2001

(first entry)

RESULT 15 AAK85886/c

AAK85886 standard; DNA; 2358 BP.

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 Matches

21;

Conservative

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Mismatches

Indels

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17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, alternative acids into a host cell to related diseases, especially and contact immune/haematopoietic related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding human immune/hematopoietic antigen polypeptides. useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                   Sequence 2358 BP; 679 A; 467 C; 345 G; 867 T; 0 other;
                                                                                                     cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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2000US-0251030.
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   Score 21; DB 22;
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Best Local :
                                                                 Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased example, they may be used to treat disorders associated with decreased
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08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
05-JAN-2001; 2001US-0259678.
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                                                                                                                                                                               Sequence 2358 BP; 679 A; 464 C; 347 G; 868 T; 0 other;
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1 agaaacaaacaaacaaa 21
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Search completed: July 31, 2002, 14:11:11 Job time: 17368 sec

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427 AGAAACAAACAAACAAACAAA 407

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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen
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Sequence 3 from Patent W00202785.
AX349065
AX349065.1 GI:18615100
                                                                                         Sprunck,S., Kluth,A., Becker,D., Luetticke,S. and Loerz,H. Promoters of gene expression in plant caryopses Patent: WO 0202785-A 3 10-JAN-2002; Aventis CropScience GmbH (DE)
                                                                                                                                                             synthetic construct.
synthetic construct
artificial sequence.
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                       /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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DNA sequence and Apodemus Unpublished
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U76839
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             Brockmann,B., Schnieders,F.,
DNA sequence divergence in a
and Apodemus flavicollis
                                                                         Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (01-NOV-1996) Max-Planck-Group, MDC for Molecular
Medicine, Robert-Rossle-Str. 10, Berlin-Buch 13125, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brockmann,B., Schnieders,F.,
DNA sequence divergence in a
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Mammalia; Eutheria;
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80. .116
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/db_xref="taxon:10116"
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Rodentia;
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Pred. No.
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Pred. No. 2.5e+02;
Mismatches 0;
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A gene,
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cyclin A gene
                         Kunze,B., Krawczak,M. and Schmidtke,J.
cyclin A gene of Apodemus sylvaticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                           Craniata; Vertebrata; Sciurognathi; Muridae;
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gene of Apodemus
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Murinae;
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Brockmann, B. Schnieders, F., Kunze, B., Krawczak, M. and Schnidtke, J. Direct Submission
Submitted (01-NOV-1996) Max-Planck-Group, MDC for Molecular Medicine, Robert-Rossle-Str. 10, Berlin-Buch 13125, Germany
                                                                                                                                                                                                                       Tao,N., Barbazuk.W.B., Liu,J., Wu,K. and Barry,G.F.
Direct Submission
Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh
Blvd., Creve Coeur, MO 63167, USA
Derived from rice genomic sequences generated from the Monsanto
Rice Genome Sequencing project. Please see
http://www.rice-research.org for more information. The sequence
data were produced primarily in the laboratories of Dr. Leroy Ho
at the University of Washington in Seattle.
Location/Qualifiers
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AV032570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                        Simple sequence repeats from Monsanto
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G
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                Similarity
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/note="intronic"
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/db_xref="taxon:4530"
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                                                                                                 /rpt_unit=aaac
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                                                                                                                              rpt_type=tandem
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Pred. No. 2.5e+02;
                Score 21;
Pred. No.
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                  2.4e+02;
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rice genomic sequences
                               Length 224;
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Primer B: CCI
STS size: 132
PCR Profile:
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Univ. OF TX Health Science Center, San Antonio
7703 Floyd Curl Dr., San Antonio, TX 78385, USA
Tel: (210)567-3842
Fax: (210)567-6781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G35045.1 GI:2358168
STS; STS sequence; primer; sequence tagged site.
human vector=pBluescript host=XL1 Blue Alu PCR products
chromosome 3 radiation hybrids cloned into pBs.
                                                                                                                                      Similarity
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Human Chromosome 3 STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 239)
ylor,S.L., Garcia,D.K., Kerbacker,K., O'Connell,P. and Stanton,V.
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                                                                                                                      Conservative
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                                                                                                                                                                                                               complement(195.
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/db_xref="taxon:9606"
83. .214
83. .100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Template:
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Kcl:
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al Vol: 20ul
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95 degrees C for 1 minute
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Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GEN Research Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp, Tel:81-886-65-2888, Fax:81-886-37-1035)
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Rattus norvegicus, OTSUKA clone, OT58.09/882h07, microsatellite
sequence, sequence tagged site.
AU026129
                                                                                                                                                                                                                                           Unpublished
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Watanabe, T.K., Hishigaki, H., Kanemoto, N., Miyakita-Mizoguchi, A., Oga, K., Okuno, S., Ono, T., Tsuji, A., Hayashi, H., Adachi, M., Yamasaki, Y., Iriye, Y., Takahashi, E., Takagi, T., Nakamura, Y. and Tanigami, A.
                                                                                                                                                                                                                                                                 Sainz
                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (tissue library: Bluescript) DNA
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2 (bases 1 to 281)
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/clone="0T58.09/882h07"
/note="0T58.09/882h07P=5'.-CGATCCTATCTCCGTGTCCTC-3',
OT58.09/882h07R=5'.-GTCATTCTCTAACTTCCACAGGTG-3'"
0T58.09/882h07R=5'.-GTCATTCTTAACTTCCACAGGTG-3'"
1 126 t
                                                                                              /tissue_lib="Bluescript"
212. .248
              /note="polymorphism"
/rpt_family="microsatellite"
/rpt_type=tandem
82 c 52 g 62 t
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                                                                                                                                    /map="22q12"
                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 2.3e+02;
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2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R. Genetic and physical mapping of simple sequence repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS; PCR primer; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site; tetranucleotide rep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence tagged sites from the human genome
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Primer B: GTCCTTGTGAGAAACTGGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e-mail: sts@corona.med.utah.edu
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49. .67
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l agaaacaaacaaacaaacaaa 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerken, S.C., Matsunami, N., Lawrence, E., Carlson, M., Moore, M., Ballard, L., Melis, R., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Rodriguez, P., Albertsen, H., Lalouel, J.-M. and White, R. Genetic and physical mapping of simple sequence repeat containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gel: Acrylamide 7%, Formamide 32%, Urea 34%
Alleles: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Annealing: 62C 10sec
Extension: 72C 20sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-mail: sts@corona.med.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Salt Lake City, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted by: Utah Center for Human Genome Research University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence tagged sites from the human genome Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STS; PCR primer; STS sequence; microsatellite marker; microsatellite repeat; repeat polymorphism; sequence tagged site.
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                                                                                                                                                                                                                                                                                                                                        polymorphism.
L12265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Denaturation: 94C 10sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR Cycles: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32P-label: B Primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer A: GATGGGAGGACTGCTTAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens DNA.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (D8S320 locus) DNA sequence, tetranucleotide repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mg++: 1mM
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                                                                      Tetranucleotide repeat polymorphism at the D8S320 locus Hum. Mol. Genet. 2, 1512-1512 (1993)
                                                                                                                        and Ward, K
                                                                                                                                            Riley,R., Nelson,L., Lu,J., Robertson,M., Ballard,L.L., Connolly,J.
                                                                                                                                                                                         Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                      tetranucleotide repeat polymorphism.
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                                                                                                                                                                   (bases 1 to 497)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                  sapiens DNA.
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                                             Location/Qualifiers
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/organism="Homo sapiens"
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HUMUT5307
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                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
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                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 100.0%; Score 21; DB 9; Local Similarity 100.0%; Pred. No. 2.2e+02;
l agaaacaaacaacaaacaaa 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: GGATATACCTGGCAATGGCAAAAAC
Primer B: GTCAATTTCCAGAGACTGTAAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gerken,S.C., Matsunami,N., Lawrence,E., Carlson,M., Moore,M., Ballard,L., Melis,R., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Rodriguez,P., Albertsen,H., Lalouel,J.-M. and White,R. Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                             Annealing: 60C
Extension: 72C
                                                                                                                                                                                                                                                                                                                                             Alleles:
                                                                                                                                                                                                                                                                                                                                                                               Mg++: 2mM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Denaturation: 94C 10sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 497)
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                                                                                                                                                    270 a
                                       Conservative
                                                                                                                                                                                                                                                                                                                                                         Acrylamide 7%, Formamide 32%, Urea 34%
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                                                                                                                                              complement(425, .449)
45 c 105 g
                                                                                                                                                                                      /standard_name="STS UT5307"
38. .62
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/clone_lib="flow-sorted chromosome 8 specific cosmid
library (LA08NC01)"
                                                                                                                                                                                                                                          /map="
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                                                                                                                                                                                                                                                                               organism="Homo sapiens"
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/rpt_unit=AAAG
45 c 105 g 62 t
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                             100.0%; Score 21; DB 11; Length 497; 100.0%; Pred. No. 2.2e+02; ative 0; Mismatches 0; Indels (
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181 AGAAACAAACAAACAAA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          287
                                                                         Local Similarity
                         1 agaaacaaacaaacaaa 21
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                                                                                                                                                                                                                                                                                Derived from dbEST (genbank accession H92026).
                                                                                                                                                                                                                                                                                                                                                                                 Buffer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitehead Institute/MIT Center for Genome Research Whitehead Institute for Biomedical Research 9 Cambridge Center, Cambridge MA 02142 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protocol
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PCR Profile:
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STS; STS sequence; primer; sequence tagged site.
human STSs derived from sequences in dbEST and the Unigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer B:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primer A: AAAGCCCTGTAAACTGAAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 617 252 1900 Fax: 617 252 1902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: thudson@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Thomas Hudson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mapped STSs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Primer: each 5 ph
dNTPs: each 4 nM
                                                                                                                                                                                                                                                                                                                                                 MgCl2: 1.5 mM
KCl: 50 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                     pH: 9.3
                                                                                                                                                                                                                                                                                                                                                                                                            Total Vol: 20 ul
                                                                                                                                                                                                                                                                                                                                                                                                                            Taq Polymerase:
                                                                                                                                                                                                                                                                                                                                  Tris-HCL: 10 mM
                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Annealing: 56 degrees C Polymerization: PCR Cycles: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermal Cycler:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Presoak:
                                                                                                                                                                                1. .150
1. .21
                                                                                                                                                complement(131. )
97 c 118
                                                                                                                                                                                                     /db_xref="taxon:9606"
/map="183.2 cR from top of Chr7 linkage group"
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Pred. No. 2.2e+02;
                                                        Mismatches
                                                                                                                                                           .150)
                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 bp
                                                                                                                                              4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA
                                                                                                                                              15 others
                                                                                 Length 503;
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STS 31-MAY-1996
                                                   Gaps
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primer_bind
primer_bind
BASE COUNT 15
ORIGIN
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G42246/c
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                                                                                                                                                                                                                                        DEFINITION ACCESSION
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                                                                                                                                                                 SOURCE
                                                                                          REFERENCE
                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                      VERSION
                                                                                                                                                                                                                                                                                            HUMUT 6478
                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                               ORGANISM
                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBMED
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                                                                                                                                                                                                                                                                                                                                                                   338
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G42246
G42246.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paavola,P., Avela,K., Horelli-Kultunen,N., Barlund,M., Kallioniemi,A., Idaenheimo,N., Kyttaelae,M., de la Chapelle,A., Palotie,A., Lehesjoki,A.-E. and Peltonen,L. High-resolution physical and generic mapping of the critical region for Meckel syndrome and Mulibrey Nanism on chromosome 17q22-q23 Genome Res. 9 (3), 267-276 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58p18t7 Human PAC clone Homo sapiens STS genomic, sequence tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G42246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Medical Genetics
University of Helsinki
Helsinki, Finland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Primer B: CCC
STS size: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Kristiina Avela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human
                              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 561)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,
Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,
Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Kristiina.Avela@Helsinki.fi
                                                                                                                                                                                STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                         Human STS UT6478, sequence
                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                            HUMUT 6478
Genetic and physical mapping of simple sequence repeat containing
                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                   Homo sapiens DNA.
                                                                                                                                                                                                                      L30582.1
                   White, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(196. .217)
1 107 c 127 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pCYPAC-1; V-type: P1-derived vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Human PAC clone"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                        GI:604976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTGTCCAGATTGGTCAGTGG
CCCTCATTTATCTGACAAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                              Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                            561 bp
                                                                                                                                                                                                                                                       61 bp DNA tagged site.
                                                                                                                              Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 552;
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JOURNAL COMMENT
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AF254660/c
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ORIGIN
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                BASE COUNT
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JOURNAL
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Best Local :
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                                                                                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                          JOURNAI
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                                                                    repeat_region
                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AGAAACAAACAAACAAA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 agaaacaaacaaacaaacaaa 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tagged sites from the human genome Unpublished (1994)
Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cycles
C 10 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C 10 sec. 64 C 10 sec. Mg++: 1.00 r 60 C 10 sec. 72 C 20 sec. Mg++: 1.00 r Gel: Acrylamide 7%, Formamide 32%, Urea 34%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e-mail: sts@corona.med.utah.edu
primer A: TACACTCCAGCCTGGGCAAC
Primer B: CTCCTCAGCAGTCTCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alleles:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     End to Label: Primer B
                                                                                                                                                                                                                                                                                                                                                                                                                               Tetrao urogallus microsatellite TUT8 sequence. AF254660
                                                                                                                                                Segelbacher,G.
Direct Submission
Direct Submission
Submitted (12-APR-2000) Unit of Wildlife Research and Management,
TU Munich, Am Hochanger 13, Freising 85354, Germany
                                                                                                                                                                                                                                                                         Segelbacher, G., \ Paxton, R. \ and \ Steinbrueck, G. \\ Characterization \ of \ hypervariable \ microsatellites \ in \ Capercaillie \\
                                                                                                                                                                                                                                                                                                                             Tetrao urogallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Calliformes; Tetraonidae; Tetrao.
                                                                                                                                                                                                                                                                                                                                                                                                                AF254660.1 GI:13926063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF254660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 100.0%; Score 21; DB 11;
Similarity 100.0%; Pred. No. 2.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial Denaturation: 94C 300sec
                                                                                                                                                                                                                                                                                                      Archosauría; Aves; Neognathae; Galliformes; 1 (bases 1 to 617)
                                                                                                                                                                                                                                                                                                                                                                            western capercaillie.
                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                            (Tetrao urogallus)
                                                                                                                                                                                                                            (bases 1 to 617)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                  62
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167. .343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /evidence=experimental complement(324...343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name="STS UT6478"
167. .186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                  /organism="Tetrao urogallus"
/db_xref="taxon:100830"
1. .617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
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                  /rpt_type=tandem
156 c 69
                                                                                                                                     Location/Qualifiers
                                                  /note="microsatellite TUT8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Denaturation Annealing Ext
64 C 10 sec. 72 C 20 sec. 30
sec. 72 C 20 sec. Mg++: 1.00 mM
                                                                                                                          .617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB DB
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                                                                                                                                                                                                                                                                                                                                                                  Match Length
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  US-09-899-718A-2
29
1 cacgcaaaggcgcg
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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000
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                         /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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4 US-09-103-840A-2
4 US-09-103-840A-1
US-08-162-809-21
US-08-162-809-19
US-08-162-809-19
US-08-162-809-19
US-08-162-809-19
US-08-325-630-1
US-09-105-537-30
US-09-105-537-30
US-09-105-33-52-3
US-09-105-33-52-3
US-08-913-362-3
US-08-913-362-5
US-08-913-362-5
US-08-913-362-5
US-08-913-362-5
US-08-913-362-5
US-08-913-362-5
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US-08-091-569-1
US-08-203-576-1
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US-08-203-576-1
US-08-203-576-1
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US-08-724-394A-20
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Compugen Ltd.
                    Sequence 9, Appli
Sequence 13, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 3, Appli
Sequence 1, Appli
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Sequence 3, Appli
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Sequence 2, Appli
Sequence 29, Appli
Sequence 1, Appli
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             Sequence
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								Q	C	a	C	O	a		C	O	
45	44	43	42	41	40	39	38	37	36	S	34 4	ω	32	31	30	29	82
15.6	15.6	15.8	15.8	15.8	15.8	15.8	15.8	15.8	16	16	16	16	16	16	16	16.2	16.2
53.8	53.8	54.5	54.5	54.5	54.5	54.5	54.5	54.5	55.2	55.2	55.2	55.2	55.2	55.2	55.2	55.9	55.9
366	240	1302	1131	1060	1060	668	541	149	80161	80161	11220	4481	623	528	205	4411529	246240
4	4	4	ω	N	H	4	4	_	4	w	4	4	4	4	4	4	N
US-09-060-756-187	US-08-884-866A-21	US-08-630-915A-17	US-08-751-512-7	US-08-690-096-11	US-07-940-605A-11	US-08-998-416-150	US-09-194-905-4	US-08-671-892A-8	US-09-370-700-1	US-09-036-987A-1	US-09-105-537-32	US-09-041-886-18	US-09-043-303-5	US-08-913-362-29	US-09-043-303-3	US-09-103-840A-1	US-08-724-394A-22
Sequence 187, App	Sequence 21, Appl	Sequence 17, Appl	Sequence 7, Appli	Sequence 11, Appl	11, 1	Sequence 150, App	Sequence 4, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 32, Appl	Sequence 18, Appl	Sequence 5, Appli	Sequence 29, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 22, Appl

### ALIGNMENTS

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; NAME/KEY:
; LOCATION:
US-08-162-809-9
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US-08-162-809-9
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; Patent No. 5457048
Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                TELEFAX: (619) 535-894
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                   TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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STREET: 4:
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l Similarity
21; Conserv
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                                                                                                                                                                                                3546 base pairs
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TD NO: 9:
               64.1%;
Score 18.6; D
Pred. No. 18;
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US-08-162-809-13
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US-08-162-809-13
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TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9949
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3591 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                      Sequence 1, Application US/09095443 Patent No. 6342593
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Best Local (
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APPLICANT: Sajjadi, Fergydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                          TITLE OF INVENTION: DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF ALP RELATED DISORDERS NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                    2408
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                                                                                                                                   APPLICANT: Plowman, Gr
APPLICANT: Peles, Eior
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STATE: California
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 84.0 hes 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P-LJ 9503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                    CGCAAATTCACGTCGGCCAGCGACG 2432
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4370 La Jolla Village Drive, Suite 700
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                                                                                                                                                                                                                                                                                                                                                                                         64.1%;
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Pred. No. 18;
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                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3591;
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; TOPOLOGY: US-09-095-443-1
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                                                                               US-09-103-840A-2
                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Patent No. 6294328
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Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2
                                                                                               OTHER INFORMATION: CDC 1551 OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or {\bf g}
                                                                                                                                                                             TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: U.S.A.
COUNTRY: U.S.A.
7 IP: 90071-2066
                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4456 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPAN: (213) 955-0440
TELEFAN: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/0. FILING DATE: June 12, 19: ATTORNEY/AGENT INFORMATION: NAME: Warburg, Richard J
                                                                                                                                                                                                                    LENGTH: 4403765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327 REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US FILING DATE: Herewith
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80.8%;
  60.0%;
75.9%;
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Pred. No.
  Score 17.4;
Pred. No. 38;
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31;
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                    Length 4403765;
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0

Matches

22;

Conservative

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Mismatches

7;

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Gaps

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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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Patent No. 5
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                 TELEPHONE: (619) 535-900
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 4411529
                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 9503
SEQUENCE
                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pasquale, Elena B. APPLICANT: Sajjadi, Fereydoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4370 La
CITY: San Diego
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nes 21; Conserv
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5457048
CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                    California : United States
                                                                                                                                                                                                                                                                                                                                                                                                      E: CAMPBELL AND FLORES
4370 La Jolla Village Drive, Suite 700
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77.8%;
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NOVEL EPH-RELATED TYROSINE KINASES,
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Pred. No. 38;
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US-08-162-809-3
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                                                                                                                        US-08-162-809-3
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                                      Query Match
Best Local Similarity 80.0
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08162809 Patent No. 5457048
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                                                                                                                                                                                                                                            TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
1613 CGCAAATTCACGTCGGCCAGCGATG 1637
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
1 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
TELECOMMUNICATION INFORMATION
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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LOCATION:
                                                                                                                                   NAME/KEY:
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                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: California
CCOUNTRY: United States of America
                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
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              cgcaaaggcgcgtcggccagccacg 27
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IDEDNESS: both
OGY: linear
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                                                                Score 17; DB Pred. No. 81;
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Pred. No.
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                                                                                                                                                                                                                                                                 Sequence 1, Application US/08460806 Patent No. 5747241
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APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
                                                                                                                                                                                                                                                                                                                                                                         1679 CGCAAATTCACGTCGGCCAGCGATG 1703
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                           NUMBER OF SEQUENCES:
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                               CITY: Arlington STATE: Virginia
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Local Similarity 80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/162,809
                  COUNTRY:
                                                                    STREET:
                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
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22202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3125 base pairs
                                                                  1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                            HARADA, SHIZUKO
HONDA, YOSHIKAZU
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                                                                                                                                                                                                             MIYAMURA, TATSUO
SAITO, IZUMU
                U.S.A.
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                                                                                                    OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT
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                                                                                                                                                           DIAGNOSTIC REAGENT FOR HEPATITIS C
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Pred. No. 81;
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US-08-460-806-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
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TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                          1185 CAGGCACAGACGCGTGCGTCAGCCAGGA 1158
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APPLICATION NUMBER: US/0
FILING DATE: 19-0CT-1994
          COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FROM PC COMPUTER: DOS
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APPLICANT: SAITO, IZUMU
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                                                                                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                  ZIP:
                                                                                                                CITY: Arlington
STATE: Virginia
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                                                                                                                                                   E: P.C.
1755 S. Jefferson Davis Highway, Suite 400
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                                                                                                U.S.A.
                                                                                                                                                                                                                                                        HONDA, YOSHIKAZU
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PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1207;
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Gaps

0;

CURRENT APPLICATION DATA:

US/08/325,630

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

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Db 11075 GGCGCGTCGGCGAGCCGCGA 11056
                                                                                                                                                               ; ORGANISM: Streptomyces venezuelae US-09-105-537-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          us-09-105-537-30/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-325-630-1
                                                                                                                                                                                                SOFTWARE: FASTSI
SEQ ID NO 30
LENGTH: 13842
TYPE: DNA
                                                           Query Match
Best Local Similarity 90.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6265202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1207 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                               APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Zue, Y.
APPLICANT: Zue, Y.
APPLICANT: APPLICANT: APPLICANT: Dao, I.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERNCE: 600.438US1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 43
NUMBER OF SEQ ID NOS: 43
SOFTMARE: PastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1185 CAGGCACAGACGCGTGCGTCAGCCAGGA 1158
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CLONE: J1-1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5750331man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,993
FILING DATE: 06-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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LOCATION:
                    9 ggcgcgtcggccagccacga 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 cacgcaaaggcgcgtcggccagccacga 28
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09105537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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2..1207
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                                                                                   57.9%;
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75.0%;
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                                                                                     Score 16.8; DB 4; Length 13842; Pred. No. 1e+02;
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                                                                      Mismatches
                                                                                   1e+02;
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10958 GCCCCGTCGCCGAGCCGCGA 10939

9 ggcgcgtcggccagccacga 28

Matches

Conservative

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Mismatches

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Gaps

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US-09-320-878-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-5
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APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REFERENCE: 600.438US1
                                                                                                                                                                                         SEQ ID NO 19
    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/09320878A Patent No. 6117659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: CIP OF 09/073,538
EARLIER FILING DATE: 1998-05-06
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1997-04-30
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER FILING DATE: 1999-02-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                  EARLIER APPLICATION NUMBER: 60/100,880 EARLIER FILING DATE: 1998-09-22 EARLIER FILING INTO NUMBER: 60/087,080 EARLIER FILING DATE: 1998-05-28 NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/105,537A CURRENT FILING DATE: 1998-06-26 NUMBER OF SEQ ID NOS: 43
                                                                                                               LENGTH: 38506
TYPE: DNA
ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 36778
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    57.9%;
90.0%;
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Score 16.8; DB
Pred. No. 1e+02;
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                          DB 3;
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                     Length 38506;
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US-08-913-362-3
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US-08-913-362-3
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                                                  Matches
                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-MAR-1995
                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
ORIGINAL SOURCE:
ORONISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60 FILING DATE: 04-AUG-1995 ATTORNEY/AGENT INFORMATION: NAME: Bent, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 710 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 17-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                / Match 56.6%;
Local Similarity 76.9%;
nes 20; Conservative
                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                     LOCATION:
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                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                       NAME/KEY:
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4 gcaaaggcgcgtcggccagccacgac 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                    mat_peptide
173..643
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116..172
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                                                    0; Mismatches
                                                                    Score 16.4; DB 4;
Pred. No. 1.4e+02;
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                                                                                   Length 710;
                                                       Indels
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4 gcaaaggcgcgtcggccagccacgac 29

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US-08-913-362-1
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                                                                                                                                                              US-08-913-362-1
                                 Query Match
Best Local :
   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13-NOV-PRIOR APPLICATION UMBER: (APPLICATION NUMBER: 17-MAR-TILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPHAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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LENGTH: 830 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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TELLEFAX: 904136
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   Score 16.4; DB 4; Length 830; Pred. No. 1.4e+02; 0; Mismatches 6; Indels
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Search completed: July 31, 2002, 12:20:34 Job time: 11657 sec

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29
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		e Ouerv			CONTRACT	v
No.	Score	Match	Match Length DB	BB	ID	Description
c 1	19.8	68.3	222	10	N46230	N46230 VV72b1
c 2	19.8	68.3	255	9	AA227176	AA227176 zr20q09.
с 3	19.8	68.3	350	10	W94459	W94459 zel2e03.rl
	19.8	68.3	984	10	BG024310	BG024310
	19.8	68.3	2306	11	BC004149	BC004149
თ	19.4	66.9	1028	10	BE733309	BE733309
7	19.4	66.9	1100	10	BE893877	BE893877
80	19.4	66.9	1829	12	AQ782504	AQ782504
ø	19.2	66.2	325	10	D48137	D48137 RICS14202A
10	19.2	66.2	1096	12	CNS04XLD	AL311818 Tetraodon
	19	65.5	290	9	AW972385	AW972385
	19	65.5	326	9	AV433974	AV433974
c 13	19	65.5	416	9	AV435705	AV435705
	19	65.5	452	9	AV430263	AV430263
	19	65.5	479	9	BB855054	вв855054
c 16	19	65.5	509	9	AV435479	AV435479
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## ALIGNMENTS

	FEATURES Source	AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 N46230/c LOCUS DEFINITION
/organism="Homo sapiens" /db_xref="GDB:3897445" /db_xref="taxon:9606" /clone="IMAGE:279069" /clone_lib="Soares_multiple_sclerosis_2NbHMSP" /sex="male" /tissue_type="multiple sclerosis lesions" /dev_stage="Age 46" /lab_host="DH10B (ampicillin resistant)"	**	Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.  The WashU-Merck EST Project Unpublished (1995) Contact: Wilson RK Washington Injuristry School of Medicine	N46230.1 GI:1187396 EST. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 222)	N46230 N46230 222 bp mRNA linear EST 14-FEB-1996 YY72b11.rl Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:279069 5', mRNA sequence.

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BASE COUNT
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       BASE COUNT
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cDNA clone IMAGE:664000 5', mRNA sequence.
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WashU-NCI human EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 1138 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 247.
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: -28ml3 revl ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 255)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
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/clone_lib="Stratagene NT2 neuronal precursor 937230"
/tissue_type="neuroepithelial cells"
/dev_stage="Ntera-2 neuroepithelial cells"
                                                                                                                                  /note="Organ: brain; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer
                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:5425859"
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                                                                                                                                                                                    /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                       /clone="IMAGE:664000"
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91.3%; Pred. No. 4.5e+02;
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COMMENT

JOURNAL

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AUTHORS

SOURCE KEYWORDS VERSION ACCESSION

FEATURES

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Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE: 358780 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ze12e03.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.llnl.gov) for further
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                                                                                                           NbHL19W."
a 107 c
                                                                                                                                                 (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by normalization to a Cot = 5. Library was constructed from the M.Fatima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung
                                                                                                                                                                                                                                  double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector
                                                                                                                                                                                                                                                                                                     /lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:358780"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Soares_fetal_heart_NbHH19W"
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  Score 19.8; DB 10; Length 350; Pred. No. 5.1e+02;
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                                                                                                             AUTHORS
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Direct Submission
Direct Submission
Submitted (01-MAR-2001) National Institutes of Health, Mammalian Submitted (01-MAR-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Tratitute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 2306)
                                                                                                                                                                                                                                                                                  Homo sapiens, clone IMAGE:2819393, mRNA.BC004149
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can be
                                                                                                           Strausberg, R
                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /Clone_lib="NIH_MGC_85"
/tissue_type="lymphoma, cell line"
/tasue_type="lymphoma, cell line"
/lab_host="DHIOB (phage resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
356 c 249 g 187 t
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                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
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                                                                                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: LLCM540 row: k column: 23 High quality sequence stop: 136.
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
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This clone has the following problem: frame shifted.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
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contact: amadan@systemsbiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
                                                                                                                                                                                                                                               CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Tissue Procurement: DCTD/DTP
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/db_xref="taxon:9606"
/clone="IMAGE:2819393"
/tissue_type="Lung, small cell carcinoma"
/clone_lib="NII_MGC_7"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
/f64 c 640 g 442 t
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3844366"
/clone_lib="NHL_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
                                                                                                                                                           Location/Qualifiers
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/db_xref="taxon:9606"
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91.3%;
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955 CACCCAAAGGAGGCCGCCCAACCACGAC 983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA Library Preparation: Life Technologies, Inc. CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE893877.1 GI:10355684
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Plate: LLAM9754 row: c column: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                         Similarity
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." a 351 c 296 g 51 t
                                                                                                                                                                                                                              Average insert size 2 kb. Technologies."
                                                                                                                                                                                                                                                                            /tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo_
                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3921346"
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Library constructed by Life
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HS_3174_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=3174 Col=20 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu plate: 3174 row: M column: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1829)
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             Unpublished (1995)
Contact: Takuji Sasaki
                                                     Sasaki,T., Miyao,A. and Yamamoto,K. Rice cDNA from callus 1995
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                                                                                                                                                                                                                                                                   RICS14202A Rice green shoot Oryza sativa cDNA, mRNA sequence
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National Institute of Agrobiological Resources
                                                                                                             Ehrhartoideae;
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L: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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                                                                                                                                                                               Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                            Bernot, A. and Weissenbacn, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish tetraodon nigroviridis
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
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305-8602,
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Similarity 80.8%;
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Location/Qualifiers
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    /clone_lib="A"
/note="Genoscope sequence ID : COAA053BC08A1-end :
1 276 c 254 g 307 t 18 others
                                                                              /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="053E16"
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                                                                                                                                                                                                     AV433974 Porphyra yezoensis TU-1 Porphyra yezoensis PM036f02_r 5', mRNA sequence.
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gametophyte of a marine red alga, Porphyra yezoensis
                Generation of 10,154 expressed sequence tags from a leafy
                                                     1 (bases 1 to 326)
Nikaido, I., Asamizu, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
                                         Tabata, S
                                                                                                                           Porphyra yezoensis
                                                                                         Porphyra.
                                                                                                  Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                        Porphyra yezoensis.
                                                                                                                                                                              AV433974.1 GI:8589199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: johng@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quackenbush,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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290 bp mRNA linear EST 01-JUN-200 EST384476 MAGE resequences, MAGL Homo sapiens CDNA, mRNA sequence. AW972385
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/note="Vector: pBluescriptSKm"
76 c 81 g 66 t
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/db_xref="taxon:9606"
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81.5%;
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Pred. No. 1.2e+03;
                                                    Nakajima, M., Nakamura, Y., Saga, N. and
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276 CGCACAGGCGCGACGGCGACGAC 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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                                                                                                                                                                                                                                                                                                                                                   yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 416)
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1: asamizu@kazusa.or.jp, URL;http://www.kazusa.or.jp/en/plant/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Porphyra yezoensis TU-1"
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/clone="PM036f02_r"
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                                                                                                                                                                                                                                                                                 /organism="Porphyra yezoensis"
/strain="TU-1"
                                                                                                                                                                                                                               /clone="PM061c04_r"
/clone_lib="Porphyra yezoensis TU-1"
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81.5%;
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81.5%;
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Pred. No. 1e+03;
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COMMENT

Contact: Yoshihide Hayashizaki

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                                                                                                                                                                                                                                                                                                       AUTHORS
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                            TITLE
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AV430263 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PL015h12_r 5', mRNA sequence.
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                          Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K., Ishii
K., Kojima,Y., Konno,H., Kouda,M., Matsuyama,T.,
Y., Ito,M., Kawai,J., Kojima,Y., Numasaki,R., Okazaki,Y., Okido,T.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Okazaki,Y., Okido,T.,
Saito,R., Sakai,C., Sakazume,N., Sasaki,D., Sato,K.,
Saito,R., Sakai,C., Sakazume,N., Sasaki,D., Sato,K.,
Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagawa
Shibata,K., Shinagawa,A., Shiraki,T., Tanaka,T., Tomaru,A., Toya,T.,
A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.,
Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.,
Ritera Faccional Salada Salad
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                        RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura,T., et al.
                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="PL015h12_r"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Porphyra yezoensis TU-1"
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81.5%;
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Search completed: July 31, 2002, 12:11:53 Job time: 13466 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   further details
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system -- 384 - format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 a
                                                                                                                                                                                                                                                                                        65.5%; Score 19; DB 9; Le flarity 81.5%; Pred. No. 1.1e+03; Conservative 0; Mismatches 5;
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/db_xref="taxon:10090"
/clone="G37002EK07"
/clone_lib="RIKEN full-length enriched, B16 F10Y cells"
/cell_type="B16 F10Y cells"
109 c 149 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                  Score
                        19.6
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18.6
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29
1 cacgcaaaggcqcqt
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67.6
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63.4
63.4
62.8
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                   0: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
2: SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA199.DAT: *
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7: /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA2001B.DAT: *
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Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cacgcaaaggcgcgtcggccagccacgac
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AAF14887
AAG90656
AAG90658
AAF74776
AAF74767
ABL18098
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Eph-related PTK Ce
Eph-related PTK Ce
Human DEC2b encodi
Human DEC2a encodi
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Human ORFX
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5	86	23	4335	60.0	17.4
phila	տ	23	4037	60.0	17.4
an cDNA se	AAH17585	22	3054	60.0	17.4
ncoding nov	822	23	2946	60.0	17.4
DNA for a	AAS34691	22	2888	0.	17.4
Ħ	6	22	2881	0	17.4
sophila me	5	23	2706	0	17.4
encoding	20	23	2556	0	17.4
A encoding nov	98	23	2322	0	17.4
coli DNA for c	N	23	1488	0.	17.4
herichia c	AAH81457	22	1488	60.0	17.4
encoding	S.	23	1440	0	7.
=	മ	23	1440	60.0	17.4
an nervous	~	22	753	60.0	17.4
encoding	AAS85709	23	728	60.0	17.4
ng nove	AAS81871	23	728	0.	7.
sophila me	ABL21553	23	636	0	7.
C glutamicum codin	AAH68531	22	349980	۲	7
m qlk	AAH20978	22	1540	61.4	17.8
	37	22	1092	61.4	
C glutamicum codin	844	22	969	61.4	17.8
tomyces	8	21	16020	62.1	
H	AAH98489	22	15214	62.1	18
<b>n</b>	21	23	14567	62.1	
nical stre	AAZ36325		10427	62.1	
tyrosi	AAC81225		9309		
Human immune/			7016		
Human immune/	AAK70464		7016	٧.	
Human immune/ha	AAK67154		7016		
Human tyrosine p	AAC81227	21	5436	2	
Human hist			5234		
Human ALP encod			4456		
Human tyrc	AAC81226		4022		

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## ALIGNMENTS

RESULT 1
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ID AAL052
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XX AAL052
XX AAL052
XX Human
XX Human;
KW Cancer
XX Homo s
XX Homo 18-APR-2000; 19-MAY-2000; 07-JUN-2000; 28-JUN-2000; 30-JUN-2000; 31-JAN-2000; 04-FEB-2000; 24-FEB-2000; 02-MAR-2000; 16-MAR-2000; 17-MAR-2000; Homo sapiens. Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds. Human reproductive system related antigen DNA SEQ ID 21-NOV-2001 (first entry) AAL05200 standard; DNA; 2473 17-JAN-2001; 02-AUG-2001. WO200155320-A2 AAL05200; gene therapy; ds. 2000US-0179065. 2000US-0180628. 2000US-01804664. 2000US-0186350. 2000US-019874. 2000US-0199123. 2000US-0199123. 2000US-0205415. 2000US-0205415. 2000US-0215135. 2001WO-US01339

NO:

7888.

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2
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2000US-0239035.

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2000US-0240960.

2000US-0241785.

2000US-0241787.
                                                             RAPER SERVICES OF 
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20-OCT-2000;
20-OCT-2000;
01-NOV-2000;
08-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                               The present invention provides the protein and coding sequences o number of human reproductive system related antigens. These can be in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoprotein of the invention.
                                                             Sequence
                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-)
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2000US-0241808.
2000US-0244617.
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RESULT 2
AALOS201/c
ID AALOS201;
XX AALOS201;
XX AALOS201;
XX ALOS201;
XX 2
AC AALOS201;
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AC AALOS201;
XX 2
DDE Human rep;
XX Human; rej;
XX W Cancer; gi
XX Human; rej;
XX 17-JAN-20;
XX 11-JAN-20;
XX 11-JAN-2
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Best Local Similarity
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        26-JUL-2000
14-AUG-2000
11-AUG-2000
11-AUG-2000
11-AUG-2000
11-AUG-2000
11-SEP-2000
01-SEP-2000
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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11-JUL-2000;
14-JUL-2000;
26-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human reproductive system related antigen DNA SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1678 CACGCAAAGGCCCGTCAGCTTGCCAC 1653
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3-JUN-2000;
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        2000US-0179065.
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2000US-01886350.
2000US-018874.
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2000US-0199123.
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2000US-0255447.
2000US-025548.
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84.6%;
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Pred. No. 44;
0; Mismatches
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      06-SEP-2000
08-SEP-2000
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20-OCTI-2000
20-OCTI-2000
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17-NOV-2000
2000US-02491786
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2000US-0241786
2000US-02411808
2000US-0241808
2000US-0241809
2000US-0246474
2000US-0246476
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2000US-0236370.
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2000US-0237037.
2000US-0237039.
2000US-0237040.
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2000US - 0233063
2000US - 0233065
2000US - 0233065
2000US - 0234274
2000US - 0234274
2000US - 0234297
2000US - 0234297
2000US - 0235484
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2000US - 0235836
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2000US - 0236368
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2000US-0231243
2000US-0231244
2000US-02312144
2000US-0231414
2000US-0231414
2000US-0232080
2000US-0232081
2000US-0232081
2000US-023298
2000US-0232397
2000US-0232398
2000US-0232398
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2000US-0239937
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
AAF14887/c
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                         Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma reesei; identification; recombination; culture condition; environmental stress; spore morphogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                              including cancer. The pre protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a
                                                                        Trichoderma
                                                                                              metabolic pathway engineering; catabolic pathway engineering; ss
                                                                                                                                                                        Trichoderma
                                                                                                                                                                                               13-MAR-2001
                                                                                                                                                                                                                        AAF14887;
                                                                                                                                                                                                                                               AAF14887 standard; cDNA; 991 BP
                                                                                                                                                                                                                                                                                                          1679 CACGCAAAGGCCCGTCAGCTTGCCAC 1654
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2474 BP; 431 A; 863 C; 812 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rsolated nucleic acid molecule encoding a reproductive system antigen
is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JAN-2001;
22-MAR-2000;
                     28-SEP-2000
                                               WO200056762-A2
                                                                                                                                                                                                                                                                                                                        1 cacgcaaaggcgcgtcggccagccac 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-465570/50.
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
2000US-0251479.
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2000US-0249245

2000US-0249264

2000US-0249265

2000US-0249297

2000US-0249299

2000US-0249300

2000US-0249300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0251856.
2000US-0251868.
2000US-0251869.
2000US-0251989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 7889; 1297pp + Sequence Listing;
                                                                        reesei.
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                        reesei EST
2000WO-US07781.
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SC,
                                                                                                                                                                                                                                                                                                                                                                       67.6%;
84.6%;
                                                                                                                                                                        SEQ ID NO:7410.
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SM;
                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                  Score 19.6;
                                                                                                                                                                                                                                                                                                                                                                                                                        368 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                    DВ
                                                                                                                                                                                                                                                                                                                                                                                    22;
                                                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                                                                                                                                    Length 2474;
                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                           Gaps
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Monitoring differential expression of genes in uses fluorescence-labeled nucleic acids isolate substrate of expressed sequence tags -
                                        array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF1147 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Asperginger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which a all specifically claimed in the present invention.
                                                                                                                                                                                                 discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on
                                                                                                                                                                                                                                                                                                                                                                 same genes in one or more second filamentous fungal cells. Monitor the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 89; Page 2992; 3161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVO ) NOVO NORDISK BIOTECH (NOVO ) NOVO NORDISK AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                 the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berka RM,
Sequence 991 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rey MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0273623
  200 A; 290 C; 269 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shuster JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INC
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    220 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enes in filamentous fungal cells isolated from the cells and a
    12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clausen IG,
                                                                                                                  from Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen
                                                                          which are
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PN FTT FER XXX
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                                                                                                                                                                                                          Matches
                                             Gallus sp
                                                             prognosis;
                                                                                    Eph-related
                                                                                                     11-NOV-1995
                                                                                                                    AAQ90656;
                                                                                                                                    AAQ90656 standard;
                                                                                                                                                                          621 CACGCAAAGGCACGTCCCCCAGTCA 597
                                                                                                                                                                                        1 cacgcaaaggcgcgtcggccagcca
                                                                                                                                                   4
                                                                                                                                                                                                                Similarity
                                                                                      PTK Cek10 cDNA
                                                                     protein
                                                                                                                                                                                                          Conservative
                                                                                                    (first entry)
                     Location/Qualifiers 2..2923
                                                                                                                                    cDNA; 3546
                                                                                                                                                                                                                64.1%;
84.0%;
                                                                      tyrosine-kinase; PTK; cancer; diagnosis;
                                                                                                                                                                                                          0;
                                                                                                                                                                                                                Score 18.6;
Pred. No. 1.
                                                                                                                                                                                          25
                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                           Indels
                                                                                                                                                                                                           0;
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.1e+02; DВ 21;

Length

991;

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W09515375-A

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RESULT
AAQ90658
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel EPH-related PTK cDNA clone Cek10 (given in AAQ90656) and a variant clone, Cek10+ (AAQ90658), whose product contains a 15-amino acid insertion in the juxtamembrane domain, were isolated from a chick embryo library in lambda gtl1. Cek10 and Cek10+ may originate from the same gene by alternative splicing. Cek10 expression was prominent in the kidney, and to a lesser extent in
        P-PSDB; AAR75710
                                                                                        07-SEP-1994;
                                                                                                           08-JUN-1995.
                                                                                                                            WO9515375-A.
                                                                                                                                                                                   Gallus sp.
                                                                                                                                                                                                    prognosis;
                                                                                                                                                                                                           Cek10+; Eph; protein
                                                                                                                                                                                                                                Eph-related
                                                                                                                                                                                                                                                  11-NOV-1995
                                                                                                                                                                                                                                                                                       AAQ90658
                                                                                                                                                                                                                                                                                                                                 2363 cgcaaattcacgtcggccagcgacg 2387
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3546 BP; 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-215256/28.
P-PSDB; AAR75708.
                                                    (LJOL-) LA JOLLA CANCER RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                           3 cgcaaaggcgcgtcggccagccacg
                                                                                                                                                                                                                                                                                                         G
                  1995-215256/28
                                  EB,
                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 63-67; 129pp; English.
                                                                                                                                                                                                     SS
                                                                                                                                                                                                                               PTK Cek10+ cDNA
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                 (first entry)
                                  Sajjadi
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                                                                       9305-0162809
                                                                                       94WO-US10140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0162809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94WO-US10140
                                                                                                                                                      Location/Qualifiers 2..2968
                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                      cDNA;
                                                                                                                                                                                                                                                                                                                                                                               64.18;
84.08;
                                                                                                                                                                                                           tyrosine-kinase; PTK; cancer; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                   A; 1100 C; 1031 G;
                                                                                                                                               a
                                                                                                                                                                                                                                                                                      3591
                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOUND
                                                                                                                                                                                                                                                                                                                                                                               Score 18.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                               .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                    673 T; 0
                                                                                                                                                                                                                                                                                                                                                                                         DB
                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                    other,
                                                                                                                                                                                                                                                                                                                                                                                        3546;
                                                                                                                                                                                                                                                                                                                                                                     0;
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AAF74776
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2408
                                                                                                                                                                     Claim 1; Page 63-68; 83pp; Japanese.
                                                                                                                                                                                                                                               DEC2 is a basic helix loop helix protein of the DEC family for use in development of drugs for treatment of disorders of cell differentiation
                                                                                                                                                                                                                                                                                                                                                                                                     Fujimoto K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200114551-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEC2a; DEC2b; bHLH type transcription factor; DEC2; DEC1; basic helix loop helix protein; cell differentiation; pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DEC2b encoding cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF74776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3591 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             originate from the same gene by alternative splicing. Cek10 expression was prominent in the kidney, and to a lesser extent in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acid insertion in the juxtamembrane domain, were isolated from chick embryo library in lambda gtll. Cekl0 and Cekl0+ may originate from the same gene by alternative splicing. Cekl0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel EPH-related PTK cDNA clone Cekl0 (given in AAQ90656) and a variant clone, Cekl0+ (AAQ90658), whose product contains a 15-am: \frac{1}{2}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF74776 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                        2001-202935/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                              AAB70693
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                                                                                                                                                                                                                                                                                                                                                                                                     Shin M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000WO-JP03991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                    drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0233286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "DEC2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      753 A; 1112 C; 1042 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64.1%;
                                                                                                                                                                                                                                                                                                                                                                                                     Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "bHLH type transcription factor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18.6;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation; proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3591;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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The present invention describes a basic hellx loop hellx (bHLH) type transcription factor designated DEC2 DEC2 can be used as a tool in the development of drugs for the treatment and prevention of disorders involving cell differentiation and proliferation. The present sequence encodes the specifically claimed human DEC2b protein, as given in the

present invention

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                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF74767 standard; cDNA; 3641 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human DEC2a encoding cDNA sequence SEQ ID NO:1.
                                                                                                                         Sequence 3641 BP; 994 A; 922 C; 836 G; 889 T; 0 other;
                                                                                                                                                     present invention.
                                                                                                                                                                             transcription factor designated DEC2. DEC2 can be used as a tool in
the development of drugs for the treatment and prevention of disorders
involving cell differentiation and proliferation. The present sequence
                                                                                                                                                                                                                         The present invention describes a basic helix loop helix (bHLH) type
                                                                                                                                                                                                                                                  Claim 1; Page 48-55; 83pp; Japanese.
                                                                                                                                                                                                                                                                                                          DEC2 is a basic helix loop helix protein of the DEC family for use in
                                                                                                                                                                                                                                                                                                                                                                                                       (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUN-2000; 2000WO-JP03991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEC2a; DEC2b; bHLH type transcription factor; DEC2; DEC1; basic helix loop helix protein; cell differentiation; proliferation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     769 aggcaaaggcgcggggggggagccgcgtc 796
                                                                                                                                                                                                                                                                                         development of drugs for treatment of disorders of cell differentiation
896 aggcaaaggcgcggggggggggcgagccgcgtc 923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 acgcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
                                                                    POCGI
                          2 acgcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                                                   2001-202935/20.
                                                                    Similarity
                                                                                                                                                                   the specifically claimed human DEC2a protein, as given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     99JP-0233286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "bHLH type transcription factor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "DEC2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.48;
78.68;
                                                                  63.4%;
78.6%;
                                                       0;
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Pred. No. 1.
                                                                    Score 18.4; DB 22; Length 3641; Pred. No. 1.4e+02;
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT

9

vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;

Human ORFX ORF2828 polynucleotide sequence SEQ ID NO:5655.

08-FEB-2001 (first entry)

AAC77273;

AAC77273 standard; cDNA; 3810

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XX PN XX
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 밁
                                                                   Matches
                                                                                               Query Match
                                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL18098 standard; DNA; 2557 BP.
1779 cccacaggcgcgtcggccatcca 1801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster genomic polynucleotide SEQ ID NO 5767.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABL18098;
                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5767; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2001
                                                                                                                                                  Sequence 2557 BP; 671 A; 546 C; 563 G; 777 T; 0 other:
                                                                                                                                                                                   at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2000; 2000US-0614150.
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                                                                                  Local Similarity
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                             3 cgcaaaggcgcgtcggccagcca 25
                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M,
                                                                   Conservative
                                                                                 62.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li PWD,
                                                                   0; Mismatches
                                                                                    Score 18.2; DB 23
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myers EW;
                                                                                                    DB 23; Length 2557;
                                                                                                                                                                                                                                                                                                                                                                                                                                              and cell-cell
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                                                                      Gaps
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CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; CC antidiabetic; hypotensive; dermatological; immunosuppressive; CC antilnflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antilnflammatory; antibacterial; antiviral; antifungal; antirheumatic; CC antilnflammatory antianaemic. The sequences can be used for determining CC the presence of or predisposition to, or preventing or treating CC pathological conditions associated with an ORRY-associated disorder. The CC nucleic actids can be used to express ORRY proteins in gene therapy CC vectors. The proteins and nucleic acids may be used to treat cancers, CC proliferative disorders, neurodegenerative disorders, osteoarthritis, CC graft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
                                                                                                                                                  Matches
                                                                                                                                                                                           Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1999;
02-APR-1999;
05-APR-1999;
1243 gccatggcggttcggccagccaccac 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
                                                                                                                                                                                                                                                                                                                   Sequence 3810 BP; 730 A; 1397 C; 1015 G; 664 T; 4 other
                                                                                                                                                                                                                                                                                                                                                                                      coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 4829-4832; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAB43064.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; contraceptive; ss.
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immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
                                                                                                                                                  Local Similarity
nes 21; Conserv
                          4 gcaaaggcgcgtcggccagccacgac
                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leach
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99US-0127636.
99US-0127728.
                                                                                                                                                                            62.1%;
                                                                                                                                          0;
                                                                                                                                                                            Score 18; I
Pred. No. 2
                                                                       29
                                                                                                                                          Mismatches
                                                                                                                                                                                                              DB
                                                                                                                                                                            .1e+02;
                                                                                                                                                                                                                 21;
                                                                                                                                                                                                      Length 3810
                                                                                                                                      0;
                                                                                                                                   Gaps
                                                                                                                                   0
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밁 20

> ΧIJ AAV81748 RESULT

11

0

AAV81748 standard; cDNA; 4456 BP

10-MAR-1999 AAV81748;

(first entry)

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                                                                        Query Match
Best Local S
Matches 21
   1471
                                                                                                                                                           Sequence 4022 BP; 776 A; 1456 C; 1081 G; 709 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 98-106; 134pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-672740/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; histidine domain-protein tyrosine phosphatase; HD-PTP; chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic; lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAB29663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200063392-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tyrosine phosphatase HD-PTP cDNA fragment cKAL16, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC81226 standard; cDNA; 4022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-APR-2000; 2000WO-JP02455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-FEB-2001
                    4 gcaaaggcgcgtcggccagccacgac 29
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gccatggcggttcggccagccaccac 1496

    Similarity
    Consert

                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99JP-0108842
                                                                                         62.1%;
                                                                        0;
                                                                                       Score 18; DB 21;
Pred. No. 2.1e+02
                                                                      Mismatches
                                                                    5
                                                                                                        Length 4022;
                                                                    Indels
                                                                    0,
                                                                    Gaps
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AAC81224
               RESULT 12
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                                                                                                               Query Match
Best Local S
Matches 21
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Markby D,
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11-JUN-1997;
11-JUN-1997;
18-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTP04; PTP05; PTP10; SAD; ALP; ALK-7; protein tyrosine phosphatase; type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma; neurodegenerative disease; neuronal survival; Alzheimer's disease; Parkinson's disease; Huntington's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                            serine/threonine kinase) are used to promote neuronal survival, particularly for treating Alzheimer's, Parkinson's or Huntington's diseases. Nucleic acid fragments of the polynucleotides encoding the proteins can be used as probes to identify and clone related sequences; to detect protein-encoded RNA; to generate transgenic animals and in gene therapy (optionally after mutation). Ab are used to determine the
                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated, enriched or purified nucleic acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The present sequence encodes human ALP. The above proteins, other than ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify substances that modulate their activity (i.e. agonists and antagonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding specific protein tyrosine phosphatases useful for identifying specific modulators for treatment and prevention of cancer and neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                   including NBP) in vivo or in vitro. These substances are used to treat or prevent diseases associated with abnormal signal transduction pathways that involve the proteins, particularly cancer (e.g. leukaemia and lymphoma), while modulators of ALK-7 (which is a type I receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-1997;
28-APR-1997;
                                                         1846
                                                                                                                                                                                       Sequence 4456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1999-009434/01.
                                                                       gcaaaggcgcgtcggccagccacgac 29
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                                                       gccatggcggttcggccagccaccac 1871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                               Similarity 80.8
21; Conservative
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97US-0044428.
97US-0047222.
97US-0049477.
97US-0049756.
97US-0049914.
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S, Peles E,
                                                                                                                                                                                       929 A; 1564 C;
                                                                                                                                62.1%;
80.8%;
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E, Plowman GD;
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Pred. No.
                                                                                                                  Mismatches
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                                                                                                                                              Length 4456;
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                                                                                                                      Gaps
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AAC81224

standard; cDNA;

20

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RESULT
AAC81227
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XEXEXXX
                                                                                                                                                                                                                                   Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200063392-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-APR-2000; 2000WO-JP02455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anticancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 58-69; 134pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-672740/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                        Sequence 5234 BP; 1049 A; 1803 C;
          Human tyrosine phosphatase HD-PTP DNA fragment cKAL11, SEQ ID
                                                                                                                                                                         2683 gccatggcggttcggccagccaccac 2708
                                                                      AAC81227
                                                                                                     AAC81227 standard; DNA; 5436
                                           23-FEB-2001
                                                                                                                                 13
                                                                                                                                                                                      4 gcaaaggcgcgtcggccagccacgac
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                     Conservative
                                           (first entry)
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                                                                                                                                                                                                                                                    62.1%;
80.8%;
                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine phosphatase cDNA,
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                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                                                    .1e+02;
                                                                                                                                                                                                                                                                                                              941 T;
                                                                                                                                                                                                                                                                  Length 5234;
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                                                                                                                                                                                                                                         Indels
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                   NO:5.
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                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human tyrosine phosphatase, histidine companies to the protein tyrosine phosphatase (HD-PTF; AAB29661) and to human companies the protein tyrosine phosphatase (HD-PTF; AAB29661) and to human companies to the protein tyrosine phosphatase (HD-PTF; AAC81263). The companies to the protein tyrosine phosphatase (HD-PTF; AAC81263) and to human companies therefore thought to contain companies to be deleted in lung cancers, and is therefore thought to contain companies to expression companies to the suppressor gene. The invention also relates to expression companies to the containing human HD-PTF nucleic acids; the creambinant production of HD-PTF; anticancer drugs containing HD-PTF; compositions containing BNA encoding HD-PTF; diagnostic containing HD-PTF oligonucleotides; antibodies specific for cuse in cancer diagnosis and investigation. HD-PTF proteins, nucleic acids cof cancers, particularly those of the lung. The present sequence corporates a human HD-PTF DNA fragment, cKALII.
                                                                                                                                                                                                   AAK67154/c
                                                                                                                                                                                                                RESULT 14
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                  2411 gccatggcggttcggccagccaccac 2436
                 WO200157182-A2.
                                                                                                                                                                                                                                                                                                                                                                Sequence 5436 BP; 1008 A; 1859 C; 1549 G; 1020 T; 0 other;
                                                                  cytostatic;
                                                                         Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                   Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21966
                                                                                                                                  06-NOV-2001
                                                                                                                                                                                     AAK67154 standard; DNA; 7016 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tyrosine phosphatase with oncostatic activity encoded by a gene frequently deleted in lung cancer, useful for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 108-117; 134pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; histidine domain-protein tyrosine phosphatase; HD-PTP; chromosome 3p21.3; gene deletion; tumour suppressor; cytostatic; lung cancer; tumour; gene therapy; diagnosis; recombinant production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAB29664.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anticancer; ds.
                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                              4 gcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                   Similarity
                                                               gene therapy; vaccine; metastasis;
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0108842.
                                                                                                                                                                                                                                                                                                                  62.1%;
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                   2.1e+02;
                                                                                                                                                                                                                                                                                                                              DB 21;
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                                                                                                                                                                                                                                                                                                                           Length 5436;
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אַרָּיאַ אָרָיאַ אָרָיאָר אָר
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22-AUG-2000

23-AUG-2000

30-AUG-2000

01-SEP-2000

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01-SEP-2000

05-SEP-2000

05-SEP-2000

06-SEP-2000

06-SEP-2000

06-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

08-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000

14-SEP-2000
        14-SEP-2000;
11-SEP-2000;
21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
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04-FEB-2000
24-FEB-2000
02-MAR-2000
16-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
07-JUN-2000
07-JUN-2000
07-JUL-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
18-AUG-2000;
22-AUG-2000;
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14-SEP-2000;
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        2000US-0235834.
2000US-0235836.
2000US-0236327.
                                              2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0225447
2000US-0225757
2000US-0225758
2000US-0225758
2000US-0225759
2000US-0226279
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2000US-0225213
2000US-0225214
2000US-0225266
2000US-0225267
2000US-0225268
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2000US-0229513.
2000US-0230437.
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2000US-0190076.
2000US-0198123.
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2000US-0232397.
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2000US-0232401.
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2000US-0232081.
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2000US-0231413.
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2000US-0224518
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2000US-0232399.
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09-AUG-2001 WO200157182-A2

17-JAN-2001;

2001WO-US01354

07-JUL-2000; 11-JUL-2000; 11-JUL-2000;

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                                                                           RESULT
                                                                                                                                                                                                            Query Match
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Matches 21
                                                                                                                                                                                                                                                                                                                                      expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK5492 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis at treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and
                                                                                                                                 3019 GCCATGGCGGTTCGGCCAGCCACCAC 2994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              metastasis
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AAK70464;
                                    AAK70464 standard;
                                                                         15
                                                                                                                                                        4 gcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to AAK64702
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                                      DNA; 7016
                                                                                                                                                                                                                               62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e the human immune/haematopoietic antigen in AAM82170 to AAM91921. (I) have cytoste
                                                                                                                                                                                                            Score 18; DB Pred. No. 2.1e 0; Mismatches
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2.1e+02;
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Human immune/haematopoietic antigen genomic sequence
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                                                                                                                      cytostatic;
                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                      gene therapy; vaccine; metastasis; ds
                                                                                                                                               (first entry)
                                                                                                                                      SEQ ID NO: 25276
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis an treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polynucleotides may be used to produce the secreted (I). By inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent,
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                                                                                                                                                                                                                                                                                                        Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
                                                                                                                                                                                                                                                                   Disclosure;
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and

SS SS SS SS Ouery Match 62.1%; Score 18; DB 22; Length 7016; Best Local Similarity 80.8%; Pred. No. 2.1e+02; Matches 21; Conservative 0; Mismatches 5; Indels diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention. Sequence 7016 BP; 1339 A; 2079 C; 2321 G; 1277 T; 0 other;

В 

0; Gaps

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Search completed: July 31, 2002, 14:11:09 Job time: 17366 sec

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Maximum DB seq length: 2000000000
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D90844 E.coli geno
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U39145 Orgyia pseu
U75930 Orgyia pseu AL021411 Streptomy AC106098 Rattus no

## ALIGNMENTS

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BASE COUNT
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AX349064
LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                  SOURCE
ORGANISM
                                                                                         FEATURES
                                                                                                                                                                                                                                KEYWORDS
                                                                                                                        JOURNAL
                                                                                                                                          TITLE
                                                                          source
                                                                                                    Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H. Promoters of gene expression in plant caryopses Patent: WO 0202785-A. 2 10-ZAN-2002; Aventis CropScience GmbH (DE)
                                                                                                                                                                                               synthetic construct. synthetic construct
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Sequence 2 from Patent WO0202785.
AX349064 GI:18615099
                                                                                                                                                                               artificial sequence.
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                        /organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"
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Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
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Aventis CropScience GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Sequence 1 from Patent WO0202785.
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                                                                                                                        Dept. of Agricultural Chemistry Oregon State University
                                                                                                                                                                                                                                           A 37-kilodalton glycoprotein from a baculovirus of Orgyia pseudotsugata is localized to cytoplasmic inclusion bodies
                                                                                                                                                                                                                                                                                                                                                                                                                             DNA polymerase; spheroidin
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                                                                                                   Corvallis, Oregon 97331-6502
                                                                                                                                                               George F. Rohrmann
                                                                                                                                                                                                                                                                                                         Gross, C.H., Wolgamot, G.M., Russell, R.L., Pearson, M.N. and
                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       D13306.1 GI:222200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polymerase and spheroidin-like protein.
                                                             Phone:
                                                                                                                                                                                  Submitted (28-SEP-1992) to DDBJ by:
                                                                                                                                                                                                                                                                                                                                                 Nucleopolyhedrovirus.
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                     rohrmann@cgrb.orst.edu 503-737-0497.
                                                               503-737-1793
Location/Qualifiers
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                                                                                                   Ahrens,C.H., Carlson,C. and Rohrmann,G.F. Identification, sequence, and transcriptional analysis of lef-3, a gene essential for Orgyia pseudotsugata baculovirus DNA replication Virology 210 (2), 372-382 (1995)
                                                                                                                                                                                                                          A 37-kilodalton glycoprotein from a baculovirus of Orgyia pseudotsugata is localized to cytoplasmic inclusion bodies J. Vicol. 67 (1), 469-475 (1993)
                                                                                                                                                                                                                                                                                                                                                                                           Orgyia pseudotsugata single capsid nuclear polyhedrosis virus
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                                                                                                                                                                                                                                                                                                           Gross, C.H., Wolgamot, G.M., Russell, R.L., Pearson, M.N. and
                                                                                                                                                                                                                                                                                                                                                                                                                   Orgyia pseudotsugata nuclear polyhedrosis virus
  pseudosugatā
                     Ahrens, C.H. and Rohrmann, G.F. The DNA polymerase and helicase genes of a baculovirus of Orgyia
                                                                                                                                                                                                                                                                                                                                                       Nucleopolyhedrovirus.
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/db_xref="taxon:10450"
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REVLPHTLCGAAANDRHALFGDKSGMDEPFHNWRPDVLYVNRYQRAHSFNVHFCPTAV
HEPSYFEVYVTKFTWDRRSPVTWNELEYIGGNGSGLVPNPGDAFCASGQLYSIPYSVP
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/protein_id="BAA02566.1"
/db_xref="GI:22202"
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Pred. No. 4.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agricultural Chemistry, Oregon 97331-7301, USA
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                                                                                                                                                                                                                                                                                                          IDPDAMPALIVOFFSDLTGRNTTHNINYRYDYNVGGALDFOPDPOPFYPYGGYWPO
PQOPPODPOCTOPPOQDPOQDPOQDPOPPOPPOPPOQDLALVOQIELSVD
EVRELOAIOLAMOQOTIWSSHATE IGTMTKILOTRVVNSAFILGAIEALQNVDRLTN
YDPNEFLRCVANETALRFEIAPDLCRVVAAFIQFFQKTHMVVKRTTFFYYVSGSLTAS
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LAQUEHAEMALATTYTALOGWEDSARORLQAANARYBEADAMSSRELDOQLVRLRPLAA
QSETLRFEKSELATENERLIGGHEDSARORLQAANARYBEADAMSSRELDOQLVRLRPLAA
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AEQNILWAGKUNEYATKTOQAAADYVAKLNAEREAYBERLJRAKDGLGAATIQRLQEEN
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KY FGVDANKRDVENFQLNTLSQYYLGDAKVDLNWQTMVEMYNNKQLGTI I KYNVQDCL
LEI ILENKLKLTDFMYSQC IMYRLCTDDF I CNISHLLSSTFHLALTNTRADPATGLT
VSDPYFFNKDDLGLMSSKGSAGLTTGMSRLRRRRI PLKDVPATAI RLCADDENVKYEG
GKVLQPRAGVYLFAFSLLDFNSLYLT MID ICACLTNLLICEDGNVYLNGDKQAI NVQL
LLQLLKCKTANIGTVEGLSNDPDLLREFGLSTLTFKVLYGDTDSTFVLPVFRREEI PEE
GRMATLGRI CAAVEARVNGLFTNGYKMAFENLMSVLILLKKKKYC Y INNNNKLVFKGW
GRMATLGRI CAAVEARVNGLFTNGYKMAFENLMSVLILLKKKKYC Y INNNNKLVFKGW
                                                                                     complement(3062. .3066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="DNA polymerase"
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1481 c 1514 g 1175 t
                                                                                                                                                                                                                                           AELRSTLDNRNREFAQGSDQFAAVNMQLNEARRAVAEKNGQLVAANEIRARLEQQLAD
ATQQLAKTEQLLVQQQKSGFMETDKQEINKEESDYLLTALDIMYKNAKILNPNLGGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence that encodes for the acids of ORF66 not shown here"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="2968. .
                                                                                                                       LKSLKEAKL'
                                                                                                                                             DNVTLSETCTQQLKSLRDDLNKNMSNVDAINDLVKTTPELDKQAIQDVRTELSKTQSR
                                                                                                                                                                               LSQNLNDLQFGLASEQRLALEQWFSTLRETTAPNDVLNFAALTNVNDLVNDLKSOIIT
KIPANMLRTFDNRIVKPEEAGAVDNVTLISAVSRLVDEYSRLGLENAQLESTNKTLYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with the sequence reported for the OPMNPV lef-3 GenBank Accession Number D45397, which contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="ORF 66; this sequence overlaps at the HindIII site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANNTFKFCLYKAQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVKKDMPVFMRVAFRAAIEQVLRHQDLSKCLDSLKANMLMYLDAFGITKPLTDYSFSM
TYNDGAGKTAADDDEAAPFKRRVITVARHCREILVNKATDFVPGNGDRIPYVLLDMQG
NVTQKAYPLRLFDAQTMRISWLKHMTILNTFNNELLEIFGDEHKDALAECYSAILEKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10450"
/note="submitter's given name: Orgyia pseudotsugata
/note=submitter's given name: Orgyia pseudotsugata
multinucleocapsid nuclear polyhedrosis virus"
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/db_xref="GI:1063689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MQHQAYDKKRAALYKIATKRKAPSASDASGKRARKGAAPSDDESGSSEDEDAPCEPKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MQRDLLSTINSMSARIKALERYEHALREIHKVIVVMRPGFNLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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OPU75930/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence update by submitter on Oct 26, 2000 this sequence version replaced gi:2934903. similar to Autographa californica nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (06-MAR-1998) Oregon State University, Chemistry, Corvallis, OR 97331-7301, USA sequence update by submitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-OCT-1996) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA 3 (bases 1 to 131995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-OCT-2000) Oregon State University, Agricultural Chemistry, Corvallis, OR 97331-7301, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ACMNPV) complete genome: GenBank Accession Number L22858.
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Virology 229 (2), 381-399 (1997)
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GALDNALVVNIVRQLCDALNDLHNATGYIHNDVKLENVLYFGARDRVYLCDYGLCKRE
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                                                                                                                                                                                                                                                                                                                                                                                                         polyhedrosis virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Orgyia pseudotsugata single capsid nuclear
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82.8%;
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Pred. No.
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complement(4742. .4975)
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                                                                                                                                                                                                                                                                                                                                                                                                             complement(5669.
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                                                                                                                                                                                                                                                                                                                                               ptp-2"
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                                                                             Query Match
Best Local :
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                                                                                       Similarity
                                    Conservative
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/note="ORF12; AcmnPV ORF13 homolog"
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/note="ORF13; le
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KTLNINSDKFISAHKSFKLEVGÅRFEQFEQRLQTLDTKLNALQCAAPTRTAPGVVFPR
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/note="ORF11;
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/protein_id="AAC59009.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TQQLQQRIKACSAGCLAGGTPPTSK" 9893. .11362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC59010.1"
/db_xref="GI:1911257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VALPRNYLAQKWFSQTAVLRHKNYVAFYTQAGLQSSDEALQARVPMVCLPMMGDQFHH
ARKLQQFGVARALDTAAVSAPQLQLAIREVIADGEAYRARIDKLRAVVEHDAAPDEKA
VKFTERVIKENNDVNWPARSLKTTAANMAYSDYFVRFPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                        translation="METAQPPISYAPPKRGAVCAYVRTVVTTTTVSDSGGNNEDRLTQ/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLERRLNESYDGAVYVSFGSGIDTNSIHAEFLQMLLDTFANLNNYTVLWKVDDAVAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORF14; egt, AcMNPV ORF15 homolog"
                                                                                                                                                                                                                                                                            /protein_id="AAC59014.1"
/db_xref="GI:1911261"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORF15; ACMNPV ORF16 homolog"
                                                                                                                                                                                                                                                                                                                                                                              /product="unknown"
                                                                                  72.4%;
                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACMNPV ORF11 homolog"
                                                                                       Pred. No. 2e+02;
                                                                                                                                Score 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lef-1,
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                                                                                                                                      DB 14; Length 131995;
                                              5
                                              Indels
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FEATURES
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                                                             source
                                                                                        prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4778(1994)) and the FramePlot program of Bibb et al., Gene 30:157-66(1984) as implemented at the true://www.nih.go.jp/
jun/cgi-bin/frameplot.pl. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, ttg or (att)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

If this cannot be identified we choose the most upstream initiation codon.

If may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 7H1 lies between 10A5 and 7B7 on the Asel-B genomic restriction fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 cacgcaaaggcgcgtcggccagccacgac 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. General contents are sequenced to the codon of the codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (URL; http://www.sanger.ac.uk/Projects/S_coelicolor/) CDS are numbered using the following system eg SC7B7.01c. SC (S. coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-JAN-1998) Streptomyces coelicolor sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof. David A. Hopwood, [3] John Innes Centre, Norwich Research Park, Colney, Norwich, Norfolk NR4 70H, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of S. coelicolor sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor sequencing at The Sanger Centre is funded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor A3(2).
Streptomyces coelicolor A3(2)
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by the BBSRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parkhill,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome Mol. Microbiol. 21 (1), 77-96 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Redenbach, M., Kieser, H.M., Denapaite, D., Eichner, A., Cullum, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          oxidoreductase; peptidylprolyl isomerase; sigma factor; transferase; xlnA; xylanase A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         abfB; aminotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor cosmid 7H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL021411.1 GI:2808758
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 35654)
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/organism="Streptomyces coelicolor A3(2)"
/strain="A3(2)"
                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Harris, D.
                                                             .35654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell, B.G. and Rajandream, M.A.
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            /transl_table=11
                                                                                                                             /gene="SC7H1.03c"
/note="sc7H1.03c"
                                                                                                                                                                                    /gene="SC7H1.03c"
                                                                                                                                                                                                                                                                QGKSPNAGGDYNSLPWRPGVLTLRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         signal sequence
                                       ′codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
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/protein_id="CAA16188.1"
/db_xref="GI:2808759"
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/gene="xlnA"
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MPIGNFPGNFGSSYTTIMSDTKANLFEGVQVYKVQGQNQYLMIVEAMGANGRYFRSFT
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/db_xref="SHISS-PROT:054161"
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/translation="MHRGSLSRGHTSAVLAAVVAALAALLVATTPAQAAGSGALR
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PGTRVQIWSCSGGANQQWRVNSDGTVVGVESGLCLEAAGAGTANGTAVQLWTCNGGGN
QKWTGLTGTPPTDGTCALPSTYRWSSTGVLAQPKSGWVALKDFTTVTHNGRHLYYGST
                                                                                                                   /note="SC7H1.03c, unknown, possible membrane protein, 391 aa; contains PS00213 Lipocalin signature, though may be spurious"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EMBL:M64551) arabinofuranosidase precursor (EC 3.2.1.55)(alpha-1-arabinofuranosidase) (arabinosidase) (478 aa), fasta scores; opt: 3129 z-score: 1807.5 E():
/product="hypothetical protein SC7H1.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="SC7H1.02, abfB, arabinofuranosidase precursor, len:
475 aa: almost identical to S. lividans TR:P96463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="SC7H1.01c, xlnA, xylanase A precursor, partial CDS, len >147 aa; almost identical to S. lividans XYNA_STRLI P26514 endo-1,4-beta-xylanase a precursor (ec 3.2.1.8) (XYLANASE A) (477 aa), fasta scores; opt: 926 z-score: 1591.1 E(): 0, 97.9% identity in 146 aa overlap. Contains N-terminal signal sequence and Pfam match to entry
                                                                                                                                                                                                                                                                                                                                                                                                                 ASSLSGSWTPQAASEGNPFAGKANSGATWTNDISHGDLVRDNPDQTMTVDPCNLQFLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95.8% identity in 477 aa overlap. Contains N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry glycosyl_hydro3 pF00331, Glycosyl hydrolases family 10, from 1 to 71, score 107.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="arabinofuranosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="overlap with cosmid St10A5"
complement(449. .453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSADRVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="mgsyalprsgvrrstrvlllalvvgvlgtatal1appgahaaes
TLGAAAAQSGRYFGTATASGRLSDSTYTSTAGREFNMVTAENEMKIDATEPQRGQFNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycosyl_hydro3 PF00331, Glycosyl hydrolases family 10, score 107.60"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A precursor (xlnA) genes from: 166 to: 2759"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="96% match to EM_BA:SLXLNA M64551 Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref-"SPTREMBL:054160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ividans arabinofuranosidase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           =="possible RBS upstream of abfB"
.2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           possible RBS upstream of xlnA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (abfB) and xylanase
                                                                                                                                        though this
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Db 31687 GCCAAGGCGCGTCGTCCATCCACGA 31663
                                                                                                       Matches
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                                                                                                                               Local
                                                  4 gcaaaggcgcgtcggccagccacga 28
                                                                                                                                 Similarity
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"SC7H1.04" possible sigma factor, len: 200 aa; some /note-"SC7H1.04, possible sigma factor; len: 200 aa; some similarity to sigma factors (ECF subfamily) from diverse organisms eg. Alcaligenes eutrophus CNRH_ALCEU B37978 rna polymerase sigma factor cnrh (191 aa), fasta scores; opt: 230 z-score: 337.3 E(): 1.4e-11, 29.5% identity in 183 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC7H1.05"
4245. .5138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="SC7H1.04"
3646. .4248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLALFALGFGALAYYGSWLRITREGTLYRLRSTAAAMQRQILRPLPLLTDDVLVDGYY
EPVQQDKLVGGDIYDVAATPWGTRVLIGDVQGKGLPAIGMAIDVVGAFREAAHREPTV
TALVDSLEAAVVRHNGYAEQRGEPERFVTAVVLGVDTGAETQLVTCGHIPPYLLHDGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="msrpsraapapaedgadqggggisirfppfrvvalvtvaatvvtv
vLgavtgtavLLigLLvfLpapasaLctprQttLvsAmvsIvvIvpvaLsteQLaDrv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="PS00213 Lipocalin signature"
complement(3426. .3431)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="SC7H1.03c"
/note="percora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RLAGHVDITAGRITHALVDDVHAFTEGPQQDDLAVLTVRRSPHRMRSPSVGEVSAAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="SPTREMBL:054162"
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/db_xref="GI:2808761"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MSDRELWARAADGDREAFGRIFDRHGKAVYNHLFRRTADWSEAE
DLTSTVFLHAWRRRADTVLDRDSALPWLLGIANGQLSNTRRRLRRAEALLHRLVSHEE
SVGDHADRVAGRIDDERRMSEIHRALARLPRHEREVVELCVWSGLDQQAAAAVLKVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          {f VTAVGAGTEHAPLGLADLVDEPRTVSWFPFPAGATLLLCTDGLTEARSPAGAFYPLET}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="putative sigma factor"
/protein_id="CAA16191.1"
                                                                                                                                                                                                                                                                           complement(5122
                                                                                                                                                                                                                                                                                                                                                                                                          PGGTSPEADFTYTDATITPIDAGTATRILSSCLGADASRYHAVVAVRTPLATEDWDGV
VVAVDSAGQYVQCQSKGDKGTSQDSPPTFINDRLWGTGRIVEYFDSMLMPAGEGKYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein SC7H1.05"
/protein_id="CAA16192.1"
/db_xref="GI:2808763"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="possible RBS upstream of SC7H1.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="SC7H1.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTVKSRLHRARRRLGADLGGAAAPPPFSSRNPVNEKEVAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                     complement(5122. .5283)
                                                                                                                                                                                                                                                                                                                                                             YDASGREIYNQAEDPKFTDEQ"
                                                                                                                                                                                                                                                                                                                                                                                     LGAGHYSSDVAKITVSYGEDPKQYPARMADGAFVYGAALSPDTPPGPRYTGPSPYVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="SC7H1.05"
/note="SC7H1.05, unknown, len: 297 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:054163"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"GI:2808762"
                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                           /gene="SC7H1.06"
                                                                                                                                                                                                                                note="SC7H1.06, unknown, len: 53 aa"
                                                                                                                                 88.0%;
                                                                                                                                                      69.7%; Score 20.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           possible RBS upstream of SC7H1.03c"
                                                                                               0;
                                                                                                                                 Pred. No.
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                        . 5283)
                                                                                                                                    5e+02;
                                                                                                                                                         DB 1; Length 35654;
                                                                                                               0;
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AC106098/c

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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCE 1 (bases 1 to 16,023)

RS MnZny D.M., Adams.C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Balsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bantooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bantooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Bantooks, S.L., Charca, M., Bryant, N.P., Buhay, C., Boutch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Chen, R., Chacko, J., Chavez, P., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Dathorne, S.R., David, M.L., Davis, C., Cox, C., Coyle, M.D., Martin, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morits, S., Moser, M., Naickerson, E., Nuckenkwo, S., Ogula, M., Wartin, R., Martindale, A., Martin, R., Martindale, A., Martin, R., Martindale, A., Maylen, A., Moser, M., Nokenkwo, S., Moyer, M., Okwuonu, G., Oragunye, N., Nickerson, E., Nuckenkwo, S., Ogula, M., Morits, S., Maser, M., Shooshtari, N., Sisson, L., Sodergren, E., Sonatke, T., Sparks, A., Stanley, H., Shooshtari, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa, A., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward.Moore,S., Warren,R., Washington,C., Walliams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D., Weinstock,G., and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-141P5, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC106098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                  findPhrapList
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                                                                                                                                                                                                                                    Center project name: GHIF Center clone name: CH230-141P5
                                                                                                                                                                                                                                                                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 162623)
Consensus quality: 126356 bases at least Q40 Consensus quality: 135615 bases at least Q30 Consensus quality: 142780 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 unordered pieces.
                                                                                                                                                  Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                     ----- Project Information
                                                                                                                                                                                                           --- Summary Statistics
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NOTE: Estimated insert size may differ from sequence length (see http://www.lbgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 74 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 19 Row: g Column: 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Ha
A.M., Holloway, M., Telford, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                          Mycobacterium tuberculosis isolate DS13 unknown sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muzny, D.M., Gibbs, R.A.
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Comparing genomes within the species Mycobacterium tuberculosis
                         Small, P.M.
                                                                                                                                               Mycobacterium tuberculosis
                                                                                                                                                                                                                         AF357175.1 GI:14009932
                                                                                                                                                                                                                                                AF357175
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                                              Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 4926)
                                                                                                                        Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                         Mycobacterium tuberculosis.
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                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTPRHPLFTSRRPPAQPTRCARKAPAVEKPDPSPRSPARTHTPR
EQPLHSAQERGRPSSGTGQPRGSQHPSGQAHVGSSLRAQRVCPALGSDLGLSSQPGAH
LLAPGIHPSAPALSLRRTPSRHPPGRQGQRSEGVSGTWMASRDRGIVISKAQPPEATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Unknown (protein for MGC:17456)"
/protein_id="AAH11138.1"
/db_xref="GI:15029830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:17456 IMAGE:3448753"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: pCMV-SPORT6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
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91.3%;
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Pred. No. 1.2e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Small, P.M., Kato-Maeda, M., Rhee, J.T., Gingeras, T.R., Salamon, H., Drenkow, J. and Smittipat, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-FEB-1998) Osamu Ohara, Kazusa DNA Research Institute, DNA Technology; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens mRNA for KIAA0589 protein, partial cds
                                                                                                                                                                                                                                                                                                                  98290545
                                                                                                                                                                                                                                                                                                                                      DNA Res.
                                                                                                                                                                                                                                                                                                                                                                     Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. IX. The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                             Nagase, T., Ishikawa, K., Miyajima, N., Tanaka, A., Kotani, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 5047)
Ohara, O., Nagase, T. and Ishikawa, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KIAA0589 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax:+81-438-52-3914)
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                                                                                                                                                                                                                                                                                                                                  large proteins in vitro 5 (1), 31-39 (1998)
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isolates"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="H37kv"
/product="KIAA0589 protein"
/protein_id="BAA25515.1"
/db_xref="GI:3043702"
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                                                                                                                                                                                                              /clone="HJ2695"
                                                            /codon_start=1
                                                                             /gene="KIAA0589"
                                                                                                                 /gene="KIAA0589"
                                                                                                                                                          /tissue_type="brain"
/clone_lib="pBluescriptII SK plus"
                                                                                                                                                                                                  /sex="male"
                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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                      Notes:

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Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk On Jun 27, 1998 this sequence version replaced gi:1449358.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C., Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E., Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T., Connor, R., Davies, R., Devlin, K., Feltwell, T., Gentles, S., Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J., Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A., Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S., Seeger, K., Skelton, S., Connocial Control of the Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Squares, S., Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Parkhill,J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis H37Rv complete genome; segment 145/162. 277165 AL123456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis H37Rv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 33818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 33818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        965 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL123456
.1 GI:3261609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RYFRELFGIRPDDYLYSLCNEPLIELSNPGASGSLFYVTSDDEFIIKTVMHKEAEFLQ
KLLPGYYMNLKQNPRTLLPKEYGLYCVQSGGKNIRVVVMNNILPRVVKMHLKFDLKGS
TYKRRASKEKEKSFPTYKDLDPMQDMEDELLLDADTSTAKTLQRDCTYLESFKIM
DYSLLLGVHNLDQHERERQAGGAQSTSDEKRPVGQKALYSTAMESIQGAARGEAIES
DDTMGGIPAVNGRGERLLLHIGIIDILQSYRFIKKLEHTWKALVHDGDTVSVHRDSFY
AERFFKEMSNTVFRKNSSLKSSPSKKGRGGALLAVKPLGPTAAFSASQIPSEREEAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAVEVETASQASDEEGAPASQASDEEDAPATDIYFPTDERSWVYSPLHYSAQAPPASD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DLRGARSYPTLEDEGRPDLLPCTPPSFEEATTASIATTLSSTSLSIPERSPSETSEQ
RYRRRTQSSGQDGRPQEEPPAEEDLQQITVQVEPACSVEIVVPKEEDAGVEASPAGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLGIGYTVGHLSSKPERDVLMQDFYVVESIFFPSEGSNLTPAHHFQDFRFKTYAPVAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="aavaarvplgrprrrpraamelevpdeaesaeagavpseaawaa
ESGAAAGLAXKAAPTEVLSMTAQPGPGHGKKLGHRGVDASGETTYKKTTSSTLKGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.3%;
91.3%;
Where possible we choose an initiation codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33818 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   875 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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REFERENCE

KEYWORDS

ORGANISM

VERSION ACCESSION DEFINITION MTCY78/c 밁 δÃ

Matches

BASE COUNT ORIGIN

COMMENT

REFERENCE

AUTHORS

JOURNAL TITLE JOURNAL MEDLINE

TITLE

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FEATURES
                                                                                                                                                                 CDS
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                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    initiation codon
/note="Rv3398c, (MTCY78.30), len: 359, GGPP synthetase, most similar to AE000797_3 Methanobacterium thermoautotrop 026156 bifunctional short chain isoprenyl diphosphate
                                                                                                                    complement(2673. .3752)
/gene="idsA"
                                                                                                                                                                                                                                                                                                                                   complement(2108. .2185)
/gene="phyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SWISS-PROT:050728"
/translation="MTEIEQAYRITESITRTAARNFYYGIRLLPREKRAALSAVYALG/translation="MTEIEQAYRITESITRTAARNFYYGIRLLPREKRAALSAVYALG/translation="MTEIEDAIRKSLDNIDDSSDPVLVALADAARRFPVPIAMFAELIDGARMEIDWTGCRDFDELIVYCRRGAGTIGKLCLSIFGPVSTATSKYAEQLGIALQQIDGARMEIDWTGCRDFDELIVYCRRGAGTIGKLCLSIFGPVSTATSKYAEQLGIALQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv3397c, (MTCY78.31), len: 302, phytoene synthase, similar to many, e.g. PSY2_LYCES P37273 phytoene synthase 2precursor (310 aa) Fasta scores, opt: 421, z-score: 500.0,E(): 6.6e-21, (32.9% identity in 295 aa overlap);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1428. .1463)
/gene="guah"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QGTLYPDVVESGGGSGTANIKSHHNVGGLPDDLKFTLVEPLRLLFKDEVRAVGRELGL
PEEIVARQPFPGPGLGIRIVGEVTAKRLDTLRHADSIVREELTAAGLDNQIWQCPVVL
LADVRSVGVQGDGRTYGHPIVLRPVSSEDAMTADWTRVPYEVLERISTRITNEVAEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="guaa"
/protein_id="CAB01027.1"
/protein_id="CAB01027.1"
/db_xref="GI:1449391"
/db_xref="GI:1449391"
/db_xref="GI:1649391"
/translation="MVQPADIDVPETPARPVLVVDFGAQYAQLIARRYREARVFSEVI
/translation="MVQPADIDVPETPARPVLVVDFGAQYAQLIARRYREARVFSEVI
PHTASITEEIRARQFVALVLSGGPASVVADGAPKLDPALLDLGYVFVDGFGYGFOAMAQA
LGGIVAHTGTREYGRTELKVLGGKHLSDLFEVQFVWMSTGDAVTAAPDGFDVVASSAG
APVAAFEAFDRRLAGVQYHEFWHTPHGQQVLSRFLHDFAGLGAQWTPALIANALIG
APVAAFEAFDRRLAGVQYHEFWHTPHGQQVLSRFLHDFAGLGAQWTPALIANALIG
ARTGARILVTVDAAFETFLEALSGVSAPEGKRKIIGRDFLRAFEGAVRDVLDGKTAEFLY
ARTGARILVTVDAAETFLEALSGVSAPEGKRKIIGRDFLRAFEGAVRDVLDGKTAEFLY
                                                                                                                                                                                                                      complement(2673.
                                                                                                                                                                                                                                                                                                                                                                                                       AALASSVTCGPAHGPLPADLGSHPSH"
                                                                                                                                                                                                                                                                                                                                                                                                                                 TNILRDVREDFLNGRIYLPRDELDRLGVRLRLDDTGALDDPDGRLAALLRFSADRAAD
WYSLGLRLIPHLDRRSAACCAAMSGIYRRQLALIRASPAVVYDRRISLSGLKKAQVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="phyA"
/protein_id="CAB01026.1"
/db_xref="GI:1449390"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(1736. .2644)
/gene="phyA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                containsPS01045 Squalene and phytoene synthases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1736. .2644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVVLDITSKPPATIEWE"
                                                                                                                                                                                                                                                                                          /note="PS01045 Squalene and phytoene synthases signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="phyA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="PS00442 Glutamine amidotransferases class-I active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(147.
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/clone="Y78"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transl_table=11
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv3400"
4885. .5673
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3775. .4821
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ARIGIPDRPAAELQDLAHYIVDRQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDPHMRPVVSYHLGWSDERGRPVNNNCGKAIRPALVFVAAEAAGADPHSAIPGÄVSVE
LVHNESLVHDDLMDRDEHRRHRPTVWALWGDAMALLAGDAMLSLAHEVLLLDCDSPHVG
AALKAISEATRELIRGQAADTARESRTDVALDECLKMAEGKTAALMAASAEVGALLAG
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/db_xref="GI:1449389"
/db_xref="SWISS-PROT:Q50727"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y09T_MYCLE (261 aa) Fastascore, opt: 1293, z-score: 1478.0, E(): 0, (74.4% identityin262 aa overlap), also similar to wmCY39.11c (34 9% identityin 238 aa overlap); Rv3400 and Rv3401 are similar to beginning and end of mCY39.11c with approx. 270aa missing fromthe middle*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv3400, (MTCY78.28c), len: 262, possible
BETA-PHOSPHOGLUCOMUTAGE, similar toseveral, e.g.
PGMB_BACSU PUTATIVEBETA-PHOSPHOGLUCOMUTAGE (226 aa, E():
1.5e-05, 33.9% identity in 245 aa overlap), also highly
similar to 000015_17 Mycobacterium laprae cosmid B1620
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RTDNDTWDLASSVGATATMIATARALASRAENPLINDPFAEPLVRAVGIDLFTRLASG
ELRLEDIGDHATGGRWMIDNIAIRTKFYDDFFGDATTAGIRQVVILAAGLDTRAVRLP
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/protein_id="CAB01024.1"
/db_xref="01:1449388"
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                                                                                                                                                                                                                              GVAAGRAGNFAVVVGINRTGRAAQAAQLRRHGADVVVTDLAELL"
                                                                                                                                                                                                                                                         DDPGAAETVYGLGNRKNDMLHKLLRDDGAQVFDGSRRYLEAVTAAGLGVAVVSSSANT
RDVLATTGLDRFVQQRVDGVTLREEHIAGKPAPDSFLRAAELLGVTPDAAAVFEDALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein Rv3400"
/protein_id="CAB01023.1"
/db_xref="GI:1449387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPPGTVVYEIDQPAVIKFKTRALANLNAEPNAERHAVAVDLRNDWPTALKNAGFDPAR
PTAFSAEGLLSYLPPQGQDRLLDAITALSAPDSRLATQSPLVLDLAEEDEKKMRWKSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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/note="Rv3401, (MTCY78.27c), len: 786, unknown, similar tomany hypothetical proteins, e.g. YVDK_BACSU HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                               WKAMFDAYLAERAERTGEKFVPFDPAADYHTYVDGKKREDGVRSFLSSRAIEIPDGSP
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                                                                                                                                                /gene="Rv3401"
                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SWISS-PROT:Q50725"
/translation="manwyrpnypevrsrvLgLpekvraCLfDLDGVLTDTASLHTKA
                                                                          /gene="Rv3401"
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/rpt_family="AluJ" 456. .744

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Db 30887 CGCAAAGCCGCGTCGGCCATCCA 30865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (26-AUG-1998) Joint Genome Institute, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere. Cosmid R32516 overlaps cosmid R31449 (AC005175) to the left from bases 1 to 8,571 of this accession, and is separated from cosmid R16815 (AC004637) to the right by approximately 5 kb. Additional chromosome 19 map and sequence information may be obtained at: http://www-bio.llnl.gov/bbrp/genome/genome.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin, J.E., McCready, P.M., Skowronski, E., Adamson, A.W.,
Lamerdin, J.E., McCready, P.M., Kyle, A., Ramirez, M., Stilwagen, S.,
Burkhart-Schultz, K., Gordon, L., Kyle, A., Ramirez, M., Stilwagen, S.,
Phan, H., Velasco, N., Do, L., Regala, W., Terry, A., Garnes, J.,
Dangganan, L., Poundstone, P., Christensen, M., Georgescu, A., Avila, J.,
Liu, S., Attix, C., Andreise, T., Trankheim, M., Amico-Keller, G.,
Coefield, J., Duarte, S., Lucas, S., Bruce, R., Thomas, P., Quan, G.,
Kronmiller, B., Arellano, A., Montgomery, M., Ow, D., Nolan, M.,
Trong, S., Kobayashi, A., Olsen, A.S. and Carrano, A.V.
Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                   /rpt_family="AluSc" 236. .286
                                                                                                                  chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                                                                                                                                       /map="19p13.3 between CDC34 and D19S342"
                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                     /note="Cosmid library constructed at LLNL from flow-sorted
                                                                                                                                                                                                                                                     /clone_lib="LL19NC03 R chromosome 19-specific cosmid
                                                                                                                                                                                                                                                                              /cell_line="5HL2-B"
                                                                                                                                                                                                                                                                                                           /clone="R32516"
                                                                                                                                                                                                                                                                                                                                                                    /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
rpt_family="L1PB1"
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91.3%;
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Pred. No. 7.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2489. .2603)

//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000"

complement(2694. .2856)
//note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 100.000"

complement(3741. .3886)
//note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: excellent, score: 100.000"
                                                                                                                                                                                                                                                                                                                                                        /rpt_family="LINE2"
complement(10187. .10279)
/rpt_family="(CGG)n"
complement(11027. .11073)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_tamily="AluJo"
9062. .9360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="LINE2"
complement(8516. .8805)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (7819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(7302. .7579)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: excellent, score: 96.000"
complement(7478. .7538)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="AluSx"
6002. .6360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_
5698.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<2487. .2603,2694. .2856,3741. .3886,4321. .4416,7302. .>7579))
4321. .4416,7302. .>7579)
/note="Hypothetical partial protein; Most similar to YB3C_SCHPO HYPOTHETICAL 60.9 KD PROTEIN C2F12.12C IN CHROMOSOME II gnl|PID|e325370 (Z97211) hypothetical protein [Schizosaccharomyces pombe]; 5'-end of
                                                                                                                      complement(12660. .12847)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5352.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
/product="R31449_3"
/protein_id="AAC32903.1"
/db_xref="GI:3461802"
                                                                                                                                               /rpt_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="RSQSPRAAAAALSQQQSLQERLRLREERKQQEELMKAFETPEEK
RARRLAKKEAKERKKREKMGGEEYMGYTRITNPFGDNNLLGTFIWNKALEKKGISHL
EEKELKERNKRIQEDNRLELQKVKQLRLEREREKAMKEQEELEMLQREKEAEHRYTWEE
QEDNFHLQQAKLRSKIRIRDGRAKPIDLLAKYISAEDDDLAVEMHEPYTFLNGLTVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical gene not discernible in genomic sequence at this time"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="(CAG)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   frame:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {	t MEDLLEDIQVYMELEQGKNADFWRDMTTITEDEISKLRKLEASGKGPG"}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="MER20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alusc"
745. .911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="Aluy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="AluJb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted exon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="LINE2"
                                                                                    _family="AluSg/x"
                                                                                                                                                                                                                                                                      _fami
                                                                                                                                                                                                                                                                                                         _family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="MLT1C"
                                                                                                                                               _family="AluSx"
                            .family="AluSx"
                                                                                                                                                                                                           .family="AluSg"
                                                                                                                                                                                                                                             .11989
   .13703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality: excellent, score: 99.000"
t(5352 .5489)
ly="LINPO"
                                                                                                                                                                                                                                                                y="AluSx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8275)
                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                              repeat_region
                                                                                                       repeat_region
                                                                                                                                                                                                                              repeat_region
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(13795. 11430) AA621023 ag03c09.s1 Soares testis NHT Homo
sapiens cDNA clone 1056208 3; Score: 856 Identity:
432/436 (99%).~(13795. 14267) At018772 ov32607.x1

Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1639044 3'
Soares_testis_NHT Homo sapiens cDNA clone 14260. .14200)
AA128938 zo11b12.r1 Stratagene neuroepithelium NT2RAMI
937234 Homo sapiens cDNA clone 56735 5'; Score: 886
Identity: 453/459 (98%).~(14913. .14564) W94459 ze12e03.r1
Soares fetal heart NbHH19W Homo sapiens cDNA clone 358780
5' Score: 668 Identity: 3457350 (98%).~(15439. .14978)
R35135 y960e12.r1 Homo sapiens cDNA clone 36877 5', Score:
766 Identity: 447/476 (93%).~(15474. .15189) AA323207
EST25973 Cerebellum II Homo sapiens cDNA clone 36877 5', Score:
530 Identity: 278/284 (97%).~Additional EST matches:
530 Identity: 278/284 (97%).~Additional EST matches:
AA975069, AA128939, AA524185, AA482347, H67626, H73320,
M78980, and many others...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M78980, and many others..."

complement(13798...>37203)

/note="Encodes human homolog of mouse
phosphatidylinositol-4-phosphate 5-kinase I-gamma"
/product="Homo sapiens mRNA for KIAA0589 protein"
/product="Homo sapiens mRNA for KIAA0589 protein"
/note="DbS similarity to overlapping ESTs:
/note="DbS similarity to overlapping ESTs:
/15645, 243707|HSCORG021 H. sapiens partial cDNA
sequence; clone c-0rg02. Score: 386 Indentity: 196/198
(98%).~(15884..15633) T31546 EST34519 Homo sapiens cDNA
end similar to None; Score: 448 Identity: 228/232
(98%).~(16081..15633) AA446775 zw89d06.r1 Soares total
fetus Nb5HF8 9w Homo sapiens cDNA clone 784139 5'; Score:
720 Identity: 377/387 (97%).~
                                                                                                                                                                                                                    complement(18117. .18182)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 2, quality: good, score: 52.000"
complement(18733. .18853)
/note="predicted exon, program: grail2exons_human_1.3,
frame: 0, quality: good, score: 68.000"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDLKGSTYKRRASKKEKEKSFPTYKDLDFMQDMPEGLLLDADTFSALVKTLQRDCLVL
ESFK INDYSLLLGVHNIDQHERERQAQCAQSTSDEKRPVGQKALYSTAMESIQGGAAR
GEA IESDDTMGGIPANMGRGBRLLLHIGIIDILQSYRFIKKLEHTWKALHDGDTVSV
HRPSFYAERFFKFMSNTVFRKNSSLKSSPSKKGRGGALLAVKPLGFTAAFSASQIFSE
REEAQYDLRGARSYPTLEDEGRPDLLPCTPPSFEEATTASIATTLSSTSLSIFBRSPS
                                                                                                          /rpt_family="Alusx"
19312. .19613
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPASDGESDT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ETSEQPRYRRRTQSSGQDGRPQEEPPAEEDLQQITVQVEPACSVEIVVPKEEDAGVEA
SPAGASAAVEVETASQASDEEGAPASQASDEEDAPATDIYFPTDERSWVYSPLHYSAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
/product="KIAA0589, partial CDS"
/protein_id="AAC32904.1"
/db_xref="GI:3461803"
/db_xref="GI:3461803"
/translation="NLNQNPRTLEPKFYGLYCVQSGGKNIRVVVMNNILPRVVKMHLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /function="putative lipid kinase"
/note="Human homolog of mouse phosphatidylinositol-
4-phosphate 5-kinase I-gamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(16781. .16783,17051. .17134,22498. .2263 25319. .25423,26521. .26553,26887. .26995,27701. .27865, 29588. .29672,30952. .31000,32239. .32322,35440. .35845, 36904. .>37203))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="DDS similarity to AA527155 ni07c01.s1 NCI_CGAP_Br2 Homo sapiens cDNA clone IMAGE:967296; Score: 958 Identity: 546/592 (92%)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AluY"
13795. .15474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16162.
                                                                                                                                                                                              _family="AluSx"
               family="AluSx"
                                                                    family="Aluy"
                                                  .19790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .16753
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vieng, C., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,Y., Beda,F., Boyuslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campoplano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC068475 175625 bp DNA linear HTG 01-JUN-2000 Homo sapiens chromosome 8 clone RP11-383B15 map 8, WORKING DRAFT SEQUENCE, 38 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 8, clone RP11-383B15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC068475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-MAY-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jun 1, 2000 this sequence version replaced gi:7677958.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 175625)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
                      Sequencing vector: M13; M77815; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 156381 bases at least Q40 Consensus quality: 166139 bases at least Q30 Consensus quality; 166136 bases at least Q30 Consensus quality; 169716 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                   Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                 Center clone name: 383_B_15
                                                                                                                                                                                                                                                                           Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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complement(21150. .21227)
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Insert size: 171925; sum-of-contigs
Quality coverage: 3.7 in Q20 bases; agarose-fp
Quality coverage: 4.0 in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently consists of 38 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. 13074 13173: gap of 13174 15155: cont. 15156 15255: gap of 15256 17626: cont 26022 26122 86600 91152 91252 57887 57986: gap of 1 57987 63137: contig of 63138 63237: gap of 1 63238 68261: contig of 49434 49533: gap of 49534 54009: cont 36995 29984 23899 11605 1 1032: contig of 1032 bp in length 103 1132: gap of 100 bp 1133 2147: contig of 1015 bp in length 2148 2247: gap of 100 bp 2248 3601: contig of 1354 bp in length 54010 54109: 44873 40557 23999 20316 6695 6794: gap of 6795 7868: con 5050 3602 3701: 256 17626: contig of 2371 bp in 1.

27 17726: gap of 100 bp
27 20315: contig of 2372 bp in 1.

16 20415: gap of 100 bp
16 21588: contig of 1173 bp in 1e.
19 21688: gap of 100 hn
9 23888: gap of 100 hn 7/968: gap of 10 9659: contig of 9759: gap of 10 23898: contig of 2210 bp in length 23998: gap of 100 bp 26021: contig of 2023 bp in length 5149: gap of 6694: con 44972: gap of 100 bp 49433: contig of 4461 bp 79822: gap of 86499: con 73256: gap of 68361: gap of 100 bp 73156: contig of 4795 ) 40556: 37094: gap of 33154: 29983: 27620: 26121: 11704: 91251: 86599: 100 bp 100 bp 1056: contig of 3362 bp 40556: gap of 100 44872: con+' 27520: cont 29883: cont 9659: contig of 1691 bp in length 1995 gap of 100 bp 11604: contig of 1845 bp in length 704: gap of 100 bp 13073: contig of 1369 bp in length 251: gap 98153: c 100 bp 33054: contig of 3071 54: gap of 100 bp 36994: contig of 3840 999: gap of 100 bp 91151: contig of 4552 bp in 09: gap of 100 bp 57886: contig of 3777 b 79722: contig of 5049: gap of 100 bp 155: contig of 1982 bp in gap of 100 km p of 100 bp contig of 6677 h p or 100 bp contig of 2263 k p of 100 bp contig of 1399 l p of 100 bp contig of 4476 bp in length of 100 bp contig of 1074 bp in length of 100 bp contig of 1545 bp in length of 100 bp contig of 1348 bp in length contig of 100 bp 100 bp f 6466 k 100 bp 100 bp 100 bp 100 bp bp in đđ bp in length þ đđ bp in length ф dα đq bp in length bp in bp in length bp in Length bp in in in length in length in in length length length length length length length length

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127864 137894: contig of 10031 bp in length
137895 137994: gap of 10031 bp in length
137995 149790: contig of 11796 bp in length
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                                                                                                                /note="assembly_fragment" 37095. .40456
                                                             40557. .44872 note="assembly_fragment"
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29984. .33054
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17727. .20315
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15256. .17626
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13174. .15155
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11705. .13073
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/db_xref="taxon:9606"
/chromosome="8"
/map="8"
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127763: contig of 10845 b
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110113: cont
                68.3%;
91.3%;
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Score 19.8; DB 2; Pred. No. 5.3e+02; 0; Mismatches 2
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2 (bases 1 to 15470)

Stover.C.K., Pham,X.-Q.T., Erwin,A.L., Mizoguchi,S.D., Warrener,P., Hickey,M.J., Brinkman,F.S.L., Hufnagle,W.O., Kowalik,D.J., Lagrou,M., Garber,R.L., Goltry,L., Tolentino,E., Westbrook-Wadman,S., Yuan,Y., Brody,L.L., Coulter,S.N., Folger,K.R., Kas,A., Larbig,K., Lim,R.M., Smith,K.A., Spencer,D.H., Wong,G.K.-S., Wu,Z., Paulsen,I.T., Reizer,J., Saier,M.H.,
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Nature 406 (6799), 959-964 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas aeruginosa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submission
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complement(999.
/gene="PA0781"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(999. .3062)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Pseudomonas aeruginosa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="PAO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .15470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:287"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:9946669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3062)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
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74 of 529 of the complete
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University Of Washington,
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CDS

gene

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YLACARYLLSEHTRGVIYPOFASHNAHTVTAILALADEÄRAAGGERDEEFORLHGM
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LVREELRGPTERNELFTEBGGFTFACVSPWNPFLAIFIGGJISAALVAGNTVLJAKPAEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STDGYTTLGASLGYNFDLGESRWLAFVKGTNLTNQTVRYASSILRDRVPAAGRGIEAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LTMGVHSRNEETARRIEELARVGNLYINRNQIGAVVGVQPFGGHGLSGTGPKAGGPNY
LLRFVSERTTSVNTTAVGGNASLLSLADAE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQLAEKPGAIATLIAETGGQNAMIVDSTALPEQVIKDAVQSAFTSAGQRCSALRVMYV
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FANVLELAVRARKLNVGITIDAEEADRLELSLELYEKLMRDPAIAGWGEFGLVIQAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SRLVQRSGEPVIRAAMNQAMKLMGKQFVLGRTISEALKNGRPCREQGYTYSFDMLGEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAATADALIRDKLSAADWQRHLGQSDNVLVNFAAWGLVMTGKVVNIDERTDGRAPSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGPDGIEAIRRNARALIETVRSRDNAVDTLDALLRQYSLDTQEGLMLMCLAEALLRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="proline dehydrogenase PutA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="putA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LELSGDYTRAKNKDTGEPLPRIAPLRLNTALIWELQQWQARVDVEHAASQHRVPEEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YIGLLASGRHRNEEGEVVAAGDDEALPEYLYSGVRADFYGVEAQDRIHLLESPYGNFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APTFYELYANGPHAATGTYEVGDADADKEKAVSTDLALRFDNGVHKGSVGVFYSRFSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(8685. .9614)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MFKASHVLQGEDQTRSAAEFFPVISANYAVDEEAYLGELLQLAD/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="putA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENRVLGLVSYAWAGFGAAFGPLVLFSLLWKRMTRNGALAGMIVGAATVILWKNLLGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WMILCLGGAVAVGFFGIAYFQAHPEQAGAVSENPERVFIELAKILFNPWIAGVLLSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:9946672"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="PA0784"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="putp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="PA0783"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .6708
                                                                                  .10379
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gene

CDS

CDS gene

CDS gene

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Matches Query Match

Local

Similarity

67.6%;

Score 19.6; DB 1; Pred. No. 1e+03; Mismatches

Length 15470; Indels

0; Gaps

0

Conservative

0;

AE008794 RESULT 15

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gene
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10750. .11913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(11918. .15043)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVAAQHLATFDSMLGAAVDPRQVPELLGLRERIRSWRFYDHFRSDAEAPARRPQIGTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="PA0786"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10389.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt NHADPWLRTALGFIGIDEVTVVAAEGEESGGRSFEDSCDEAEQRLLALARSA}^*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              codon_start=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(11918. .15043)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MAWFHLLVAAAFEVAFAMGMKFSNGFGRLWPSLLTVVAAIGGIY/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                 {	t LSQVGKMLGFSAHSSGGSTLATQIEKYRHSAEGRTGSIGDKLRQMLSASVRSYREGPA}
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	CDS	gene	FEATURES Source				JOURNAL COMMENT	JOURNAL PUBMED REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE	SOURCE	LOCUS DEFINITION ACCESSION VERSION
(AAC75121.1); Blastp hit to AAC75121.1 (732 aa), 878 identity in aa 13 - 732" /codon_start=1 /trans1_table=11 /trans1_table=11 /product="putative tyrosine-protein kinase in colanic acid export" /protein_id="AAL21020.1" /protein_id="AAL21020.1" /db_xref="G1:16420650" /trans1ation="MTEKAKQSAAVTGSDEIDIGRLVGTVIEARWHVLGTTAIFALCA VIYTFFATPIYSADALVQIEONAGNSIVQDINSALANKPPASDAEIQLIRSELVLGKT VDDLDLDIAVTKNTFPLFGAGWERLMGRHNEMVKVTTFTRDETMSGQIFTLKVLGDKR YQLVSDGGFSAQGVVGQPLNKDGVTMRVEAIDARPDTEFTVSKFSTLGMINNLQNNLT	/note="STW2116" complement(682227) /gene="wzc"	/organism="Salmonella typhimurium LT2" /strain="LT2; SGSC 1412; ATCC 700720" /db_xref="ATCC:700720" /db_xref="taxon:99287" complement(682238) /gene="wzc"	This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistries or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one ml3 subclone.  126591	The analyses of ribosome binding sites and promoter binding sites were kindly provided by Heladia Salgado, Julio Collado-Vides and ReguonDB; http://kinich.cifn.unam.mx:8850/db/regulondb_intro.frameset	EC numbers were kindly provided by Junko Yabuzaki and the Kyoto Encyclopedia of Genes and Genomes; http://www.genome.ad.jp/kegg/, and Pedro Romero and Peter Karp at EcoCyc; http://ecocyc.PangeaSystems.com/ecocyc/	Coding sequences below are predicted from manually evaluated computer analysis, using similarity information and the programs; GIIMMER; http://www.tigr.org/softlab/glimmer/glimmer.html and GeneMark; http://opal.biology.gatech.edu/GeneMark/	Submitted (29-MAR-2001) Genome Sequencing Center, Department of Genetics, Washington University School of Medicine, 4444 Forest Park Boulevard, St. Louis, MO 63108, USA Supported by NIH grant 5U 01 AI43283	Nature 413 (6858), 852-856 (2001) 11677609 2 (base 1 to 26591) The Salmonella typhimurium Genome Sequencing Project. Direct Submission	A (bases 1 to 26591)  MCClelland,M., Sanderson,K.E., Spieth,J., Clifton,S.W.,  MCClelland,M., Sanderson,K.E., Spieth,J., Dante,M., Du,F.,  Latreille,P., Courtney,L., Porwollik,S., Ali,J., Dante,M., Du,F.,  Hou,S., Layman,D., Leonard,S., Nguyen,C., Scott,K., Holmes,A.,  Grewal,N., Mulvaney,E., Ryan,E., Sun,H., Florea,L., Miller,W.,  Stoneking,T., Nhan,M., Waterston,R. and Wilson,R.K.  Complete genome sequence of Salmonella enterica serovar Typhimurium  LT2	Salmonella typhimurium LT2. Salmonella typhimurium LT2. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.	AE008794 26591 bp DNA linear BCT 25-OCT-2001 Salmonella typhimurium LT2, section 102 of 224 of the complete AE008794 AE0086468 AE008794.1 GI:16420649
gene RBS CDS	-35_signal	RBS -10_signal			CDS	RBS gene			CDS Gene		

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membrane"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(2679.
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acid export"
                                                                                                                                                                                                                                                                                                                                                                                                                  'gene≖"wza"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="wzb"
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DQNOIQVKGVILNSIFRRATGYQDYGYYEYEYQSDSK"
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gene CDS

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Search completed: July 31, 2002, 14:00:49 Job time: 17491 sec
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Best Local S
Matches 22
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l Similarity 84.6%;
22; Conservative
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OGAN
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Result
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ALIGNMENTS

## RESULT 1 US-08-941-445A-4 Sequence 4, Application US/08941445A Patent No. 6107060 GENERAL INFORMATION: APPLICANT: Keeling, Peter APPLICANT: Guan, Hanping CLASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 60/026,855 FILING DATE: 30-SEP-1996 ATTORNEY/AGENT INFORMATION: NAME: Winner, Ellen P REGISTRATION NUMBER: 28,547 REFERENCE/DOCKET NUMBER: 89-97 TELECOMMUNICATION INFORMATION: TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 4800 base pairs COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: JEP PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Rela CURRENT APPLICATION DATA: APPLICATION NUMBER: US, FILING DATE: 30-SEP-199 CORRESPONDENCE ADDRESS: ADDRESSEE: Greenlee, Winner and Sullivan, P.C. STREET: 5370 Manhattan Circle FEATURE: APPLICANT: Guan, Hanping TITLE OF INVENTION: Starch Encapsulation NUMBER OF SEQUENCES: 37 ORIGINAL SOURCE: MOLECULE TYPE: DI NAME/KEY: LOCATION: LOCATION: LOCATION: STREET: 5370 M CITY: Boulder STATE: CO STRANDEDNESS: ORGANISM: TYPE: nucleic acid TELEPHONE: ZIP: 80303 US PatentIn Release #1.0, Version #1.30 CDS not relevant join(1449..1553, 1685..1765, 1860..1958, 2055 ..2144, 2226..2289, 2413..2513, 2651..2760, 2858 ..3101, 3212..3394, 3490..3681, 3793..3879, 3977 Zea mays (303) 499-8080 double 30-SEP-1997 DNA (genomic) US/08/941,445A

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                                                                                        CORRESPONDENCE ADDRESS: ADDRESSE: Greenlee, Winner and Sullivan,
                                                                                                                                APPLICANT: Keeling, Peter
APPLICANT: Guan, Hanging
TITLE OF INVENTION: Starch Encapsulation
NUMBER OF SEQUENCES: 37
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CITY: Boulder STATE: CO COUNTRY: US ZIP: 80303
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US-08-679-645-25

Sequence 25, Application US/08679645 Patent No. 6350934

GENERAL INFORMATION:

APPLICANT:

APPLICANT: APPLICANT:

Merlo,

Patricia Ann

Owens

McSwiggen, James A Zwick, Michael G. Edington, Brent E.

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 499-8089 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
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                                                                                                                                                                                                                                           3241 cccggcg-----gatgcggcgctcggcatgaggactgtcgggagcgagcgcgccccaaa 3294
                                                                                                                                                                                                                                                                                                                       3196 cgacagat-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CL
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                          629
                                                                                                                                                                                                                 569
                                                                                                                                                                                                                                                                                       509
                                                                                                                                                                                                                                                                                                                                                        449 CACCATGTCGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGC 508
746 CGGCGGCCTCGGTGACGTCCTCGGTGGCCTCCCCCCTGCCATGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 30-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Winner, Ellen P
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                    tggcggcctcggcgacgtcctcggggggcctccccgccgccatggccg
                                                                                       gggcagcggcggcatgaacctcgtgttcgtcggcgcccgagatggcgccctggagcaagac 3414
                                                                                                                                                           gcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtggtgcgccac 3354
                                                                                                                                                                                                                                                                                     CGACAGGTCGGCGCCGTCGTCGCTCCGCCACGGGTTCCAGGGCCTCAAGCCCCGCAG 568
                                                                        ---CGGCGCCGGCATGAACGTCGTGTTCGTCGGCCGAGATGGCCCCCTGGAGCAAGAC
                                                                                                                                         GCAGCAGCGGTCGGTGCAGCGTGGCAGCCGGAGGTTCCCCTCCGTCGTCGTGTACGCCAC 688
                                                                                                                                                                                                               241;
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69.5%;
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Pred. No. 4.2e-23;
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US-08-679-645-25
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Matches 221; Conserv
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TITLE OF INVENTION: M
TITLE OF INVENTION: I
NUMBER OF SEQUENCES:
3196 cga-----cagattccggcgtccaggttttcagggcctgaggccccggaacccggcgga 3249
                                                                                                                                                                                                                                                                                                         3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                           3250 tgcgg-----cgctcggcatgaggactgtcggagcgagcgcccccaaagcaaagcag 3303
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LENGTH: 2267 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: September 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/6
FILING DATE: July 12, 1996
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
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TELEX: 67-3510
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FILING DATE: July 13,
APPLICATION NUMBER: 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Californ: COUNTRY: U.S.A. ZIP: 90071-2066
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STREET: Suite 470
CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                      GCAGCAGCAGCAGCGCGCGCGGGGCCAGGTTCCCGTCGTCGTCGTGTGCGCCAGCGC 412
                                                                                                        gaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcgg 3363
                                                                                                                                           California
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Skokut, Thomas A
Young, Scott A.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Folkerts, Otto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYSTEM: IBM P.C. DOS 5.0
Word Perfect 5.1
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                                                                                                                                                                                                                                                                                                                                                                              3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOSITION AND METHODS FOR MODULATION OF GENE EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                           Score 118.8; DB 4;
Pred. No. 1.2e-18;
0; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                               Length 2267;
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                                                                                                                                                                                                                                                                                                         Query Match 2.2%;
Best Local Similarity 57.8%;
Matches 247; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                           3425
                 3539 gcaggccaacggtcaccgggtcattggtcattctccccgcgctacgaccagtacaaggacgc 3598
                                                                                                       3484 tataaatgittcitccigcagccaigccigccgitacaacgggtgccgigtc----cgi 3538
                                                                                                                                                                                                                                                 3365 ggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcgcgctc 3424
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LENGTH: 2549 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Crane-Feury, Sharon E
REGISTRATION NUMBER: 36,113
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       172
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PRIOR APPLICATION NUMBER: US 08/070,455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF TITLE OF INVENTION: POTATO TO FORM AMYLOPECTIN-TYPE STARCH
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                                                                                                                                                                                                                         112 GGAATGAACTTGATCTTTGTGGGTACTGAGGTTGGTCCTTGGAGCAAAACTGGTGGACTA 171
292 TTAGGCCCGCGGACATCGGGTAATGACAATATCCCCCCGTTATGACCAATACAAAGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 CGGCGACGTCCTCGGCGGCCTGCCGCCGATGGCCGCGAATGGGCACC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2549 base pai
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Virginia
COUNTRY: United (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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SOFTWARE: PatentIn Release #1.0,
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                                                                                                                                                                       9909ac9tcctc999999cctcccc9cc9ccatggccgtaag-cttgcgccactgccttct 3483
                                                                         CCTACTCATTCATTACTTATTTTGTTTAGTTAGTTTCTACTGCATCAGTCTTTTTATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (703)
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SYSTEM: PC-DOS/MS-DOS
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703) 836-2021
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                                                                                                                                                                                                                                                                                                                         Score 83; DB 1;
Pred. No. 3.9e-10;
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                                                                       Matches
                                                                                                         Query Match
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                                                                                                                                                                                                                                                                               TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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                 3365 ggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcggcctc 3424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: GENETICALLY ENGINEERED MODIFICATION OF TITLE OF INVENTION: POTATO TO FORM AMYLOPECTIN-TYPE STARCH
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1437
                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/070,455 FILING DATE: 09-JUN-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Virginia
                                                                                         Local
                                                                                                                                                                                                           TOPOLOGY: lin
                                                                                                                                                                                                                                         LENGTH: 4964 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Crane-Feury, Sharon REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/470,720
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                                                                                           Similarity
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WIKSTROM, Olle
TALLBERG, Anneli
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                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                           linear
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                                                                                         2.2%;
57.8%;
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                                                                                         Score 83; DB 1;
Pred. No. 5.3e-10;
                                                                       Mismatches 165; Indels
                                                                                                         Length 4964;
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                                                                                           TELEFAX: (619) 235-01:
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                         REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
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TOPOLOGY: 1 MOLECULE TYPE:
                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Newport Beach
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                              STRANDEDNESS:
                                                 TYPE:
                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE: 10-SEP-1993
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                              LENGTH:
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                                               nucleic acid
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620 Newport Center Drive 16th
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Wellems, Thomas E.
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Miller, Louis H.
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               linear
                                                                                                                             (619) 235-8550
                                single
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AND PLASMODIUM FALCIPARUM ERVTHROCYTE BINDING PROTEINS: 45
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HYPOTHETICAL: ANTI-SENSE:

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US-08-232-463-14/c
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         Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL IMPORMATION:
APPLICANT: DORNER, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                           16186 TATATGTGTATGTATATGTATTTAGGTATTATATATGTGTTTGTTAATGTATATATGT 16127
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  APPLICANT:
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                                                                                                                                                                                                                             611 aaaactttagtattttgattgtgtttttagtttttatttcattttgtttcttttaaggg 670
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                                                                                                             789 gcaaactttatcattatttgtctaaattaattttttct 826
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SCHEIFLINGER,
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Best Local s
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1795 atgtgccaggctgccagccgctccgcggtaccactagtctcgta
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IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)863-4109
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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CITY: A
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Local Similarity 4.5%; Pred. No. 1.3e-05;
nes 18; Conservative 232; Mismatches 15
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OPERATING SYSTEM:
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                                           gcacgcaaaggcgcgtcggccagccacgacgccgctggaaagcgcgccggcgaaccgaga 1794
                                                                                                    ggcgagagcgagagcacacatggcccccagaactgaaagcgagggagcacacgagaaggc 1614
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                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 14:
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TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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IMMEDIATE SOURCE
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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                                                                                                     442 tttatgcctcatttggaaatttcgttttgaaaattatgctagtacacacttattcttgta 501
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                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 22313-0299
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                                                                                                                                                                                                                                                                                y Match 1.6%; Score 62.2; DB 1; Length 7218; Local Similarity 4.8%; Pred. No. 5.3e-05; hes 19; Conservative 225; Mismatches 153; Indels 0
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STRANDEDNESS: sing
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1800 Diagonal Road, Suite 500
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US-07-867-106-2
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                                                   Matches 214; Conservative
                                                              Query Match 1.6%; Score 58.8; DB 1; Length 5852; Best Local Similarity 49.1%; Pred. No. 0.0003;
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APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
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ATTORNEY/AGENT INFORMATION:
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CITY: Philadelphia
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Williams, Keith L
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US-08-998-416-595
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INFORMATION FOR SEQ ID NO:
                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,
                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                REGISTRATIÓN NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                                APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997
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CITY: Research Triangle Park
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Knechtle, Philipp
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Steiner, Sabine
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US-07-867-106-2/c
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                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/07867106 Patent No. 5389526
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                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                      ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                    TITLE OF INVENTION: Improved Plasmid Vectors for Cellular TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium NUMBER OF SEQUENCES: 19
                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. STREET: One Liberty Place 46th Floor
                                                                                                                                                                                                                                                   APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith
               CURRENT APPLICATION DATA:
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ORIGINAL SOURCE:
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LENGTH: 658 base pairs
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                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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OTTMY: Philadelphia
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                                                                                                                      COUNTRY:
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US/07/867,106
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                             Version #1
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PRIOR APPLICATION DATA:

FILING DATE:

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                                                                                   US-08-947-823-1
                             Sequence 1, Application US/08947823 Patent No. 6114605 GENERAL INFORMATION:
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Matches 228; Conserv
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LENGTH: 5852 base pairs
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 APPLICANT:
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LOCATION:
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
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                                                                                                                                                                                                                     CCAGGCAAAATAAACAGCATCAGAAATCTCATTAAATGTTGGTCTCAAAAAGTTTTATTAA
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 Isgouhi
                   Valerie M.
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Pred. No. 0.0011;
0; Mismatches 236;
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Best Local Similarity
Matches 238; Conserv
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FILLING DATE: 09-OCT-15
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC
FILING DATE: 09-OCT-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
                                                                                                                                              13140 TACTCTTAATATTCATAACTCTCATCTTTTCATATTCATAACCTCCAAATATTTAAACTA 13159
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TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Pest Resistance in Plants
                                                                                                                                                                                                                                                                                              13020 TGCTTAATTACATGATAAAAACTTTAGTTGTTCTTTTTACATGGTTTGCTAACTTTAATT 13079
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60 FILING DATE: 10-OCT-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                   185 acctaagaggaaattcagttttatactagttttcagttttattattgtttattaagtgttt 244
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CITY: San Francisco
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REGISTRATION NUMBER: 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                                           AACCCCTACCAAGATTATTAGGCTATTATTTTTATTCTATAGTAAAAACAAATGATGAA 13319
                                                                        AAACTTTAAGATATCTTTTGATATTTGTTCAATAATAAATTCAACTTCTTTATCTTATGA 13259
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 55.6; DB 3; Pred. No. 0.005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              304;
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US-08-998-416-186
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   Query Match 1.4%;
Best Local Similarity 46.1%;
Matches 217; Conservative
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                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: CH 0016/9
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/9
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INFORMATION FOR SEQ ID NO:
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                                                                                              ORIGINAL SOURCE:
ORGANISM: PAG
                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Research Triangle Park
No. 6239264th Carolina
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Steiner, Sabine
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Knechtle, Philipp
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Score 54.2; DB 4;
Pred. No. 0.0013;
0; Mismatches 253;
                              Length 615;
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US-08-998-416-1137
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Sequence 1137, Application US/08998416 Patent No. 6239264
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            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,24
REFERENCE/DOCKET NUMBER: F
                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 24-DEC
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Knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES
VENTION: AND USES THEREOF
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Steiner, Sabine
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IBM PC compatible
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No. 6239264artis Corporation
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N: 435
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                               38,241
            PF/5-30306/A/CGC1976
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                                                                                                                                                        Sequence 288, Application US/08998416 Patent No. 6239264
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Best Local 9
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                                                                                                                                         GENERAL INFORMATION:
                                             APPLICANT:
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ORIGINAL SOURCE:
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TITLE OF INVENTION: GENOMIC DNA SEQU
                                APPLICANT:
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                                                                                                                                                                                                                                                  598 AAAATATTATAAAGAATGTAGTTAAAAATACTTATAAAA 636
                                                                                                                                                                                                                                                                              725 aactcaacttttatatgcttattcgtgcatattataaaa 763
                                                                                                                                                                                                                                                                                                              665 taagggaaataccaatgccactaatccattccatcttagaaaaatctctttatcttacaaa 724
                                                                                                                                                                                                                                                                                                                                                                        605 gcttagaaaactttagtattttgattgtgttttagtttttatttcattttgtttcttctt 664
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919-541-8689
                                                                                        Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
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                                           Wendland, Jurgen
Knechtle, Philipp
            Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                            Mohr, Christine
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LENGTH: 837 base pairs
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607 ttagaaaactttagtattttgattgtgttttagtttttatttcattttgtttcttcttta 666
                                     436 tactaatttatgcctcatttggaaatttcgttttgaaaa-----ttatgctagtac 486
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                                                                      487 acacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcattctgta 546
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road CITY: Research Triangle Park
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258;
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1;

- βb 478 ACTTTAATTTCTTATTAATTTTTATATTATTTAATAAATTATATTTCATTTTATTTA 537
- Qy
- Db
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- В

Search completed: July 31, 2002, 12:17:49 Job time: 11492 sec

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1)

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2002, 08:27:27; Search time 5855.71 Seconds (without alignments) 8724.130 Million cell updates/sec

Sequence: Perfect score: US-09-899-718A-1 3785 1 gtttggtttcgctgtttttc.....tggaccgcgtgttcgtcgac 3785

Scoring table:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:* em_esthum:* em_estba:*

5: 6: 7: 7: 10: 113: 114: 115: gb_estl:*
gb_est2:*
gb_htc:*
gb_sts:*
gb_sts:*
em_gss_hum:*
em_gss_inv:*
em_gss_pin:* em_estpl:*
em_estro:*
em_htc:* em_estov:* em_estmu:* em_estin: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_vrt:*

## SUMMARIES

Result No. 1 2 3	Score 325.8 325.8 293.4 293.2 291.6	Query Match 8.6 7.8 7.7	Query Query Match Length Match 527 7.8 579 7.7 558 7.7 638	DB 100	ID AW448831 BE402419 BE602243 AL508959
<b>-</b> ω	293.2	7.7	558	10	BE602243
4 70	283.8	7.5	639 639	10	AL508959 BE414303
6	278.8	7.4	700	ا و	AL508163
7	258.8	6.8	513	9	AL508933
8	248	6.6	677	10	BE414500
9	247	6.5	700	و	AL506567
10	231.4	6.1	444	10	BM368238
11	220.6	5.8	494	ø	AW448811
12	210.2	5.6	462	ø	AL506396
13	178.4	4.7	375	9	AW448845
c 14	118.6	3.1	1885	10	BE420745
c 15	114	3.0	1135	12	CNS033GQ
16	112	3.0	879	12	CNS01JRG
17	111.8	3.0	470	10	C73133

γ

Query Match 8.6%; Best Local Similarity 99.4%; Matches 327; Conservative

Score 325.8; DB 9; Length 527; Pred. No. 5.5e-38; 0; Mismatches 2; Indels 0

Indels 0; Gaps

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443 443 45	34 35 35 36 37 38 39	30 31 32 33	22 24 25 26 28	18 19 20 21
101.6 101.6 101.2 101	102.8 102.6 102.6 102.6 102.4 102.2 101.8	104.2 104 104 103.6 103.2	109.4 106.4 106.2 105.8 105.4 104.6	111.4 110.4 110.2 109.4
22.7			 	
855 855	848 870 1139 1223 924 1185 656 1309	982 834 1184 614 960	896 1198 1101 1317 1317 964 1101	1036 1059 907 855
12 12 12	3 12 12 10 10 10	122	12 12 12 12	12 12 12
CNS04RQH BM415686 AQ324474 AZ183849	BI644518 AQ330286 AQ897537 B12981 BM415947 BF273407 CNS01ZJA BE420736	AQ325799 B12387 B1317 CNS0152H AG031602	BM415641 B08337 CNS012JN BE420688 BM416130 CNS0153V CNS00KB5	CNS03LWJ CNS00Z2B CNS021J4 B1645015
	N O	9 N	BM415641 OP20719 M B0837 T19F9-Sp6.1 AL101645 Drosophil BE420688 HWM001.E0 BM416130 OP21217 M AL104965 Drosophil AL077453 Drosophil	AL250012 Tetraodon AL097133 Drosophil AL176953 Tetraodon Bi645015 OP2815 Mi

## ALIGNMENTS

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/db_xref="taxon:4565" /clone="p56-1p"	
/cultivar="Wyuna"	
	source
Location/Oualifiers	FEATURES
Final : of a cost of the cost	
Fav: 61 2 6246 5000	
GPO Box 1600, Canberra, ACT, Australia	
.I.R.O.	
Division of Plant Industry	
Contact: Bryan Clarke	COMMENT
Unpublished (2000)	JOURNAL
Genes active in developing wheat endosperm	TITLE
Clarke, B.C., Hobbs, M. and Appels, R.	AUTHORS
1 (bases 1 to 527)	REFERENCE
; Triticeae; Triticum.	
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
Triticum aestivum	ORGANISM
bread wheat.	SOURCE
EST.	KEYWORDS
AW448831.1 GI:12019366	VERSION
	ACCESSION
BRY Triticum aestivum cDNA clone P56-1P, mR	DEFINITION
AW448831 527 bp mRNA linear EST 03-JAN-2001	LOCUS
	AW448831
	RESULT 1

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                                                                                                                                                                                                                                                                                                                                             Contact: Appels R
Div. of Plant Industry, CSIRO
Canberra ACT 2601 AUSTRALIA
Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                                                                                                                                                                                                                                                                                         International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
                                                                                                                                                                                                                                                                                      Email: rudi@pi.csiro.au
International Triticeae EST Cooperative
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquemin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.
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(bases 1 to 579)
       109
/note="Vector: Lambda zap/Bluescript; Site_1: XhoI; Site_2: EcoRI; Plants grown in Phytotron with 18C/13C (day/night) 16 hour light. M13 Reverse sequencing prin used 1.0 Kbp average insert size."

207 c 189 g 72 t 2 others
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                                                                                                                                                                                                                                   organism="Triticum aestivum"/
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cacqggcagcggcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaa 3411
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                                                                                                                                                                                                                                                                                      100 Jordan Hall, (Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE602243
558 bp mRNA linear EST 22-OCT-2001
HVSMEh0098D06f Hordeum vulgare 5-45 DAP spike EST library
HVCNNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0098D06f,
                                                                                                                                                                    High
                                                                                                                                                                                                                                        Email: rwing@clemson.edu
Total hg bases = 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 558)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D.,
Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fento,
R.D., Close,S.J., Oates,R. and Main,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9859804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development of a genetically and physically anchored EST for barley genomics: Morex 5-45 DAP spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                 Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                               Clemson University
                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE602243.2 GI:13189982
                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Triticeae;
                                                                                                                                           quality sequence start: 16 quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
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/clone_lib="Hordeum vulgare
                    /clone="HVSMEh0098D06f"
                                             /db_xref="taxon:4513"
                                                                      /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                           . 558
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88.3%;
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                                                                                                                                                                                                                                                                                                                                           Clemson,
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  5-45 DAP
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spike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choi, D.W., Fenton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  579;
     EST library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3276 gagcgaccgcccaaagcaagcaggaaaccgcaccgattcgaccggcggtgcctct 3335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 GTTTTCAGGCCTCAGGCCCCGGAACCCGGCGGATGCGCTTGGTATGAGGACTATCG 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                   3395 ccatgftgtgcgcgccacgggcagcggcgatgaacctcgtgttcgtcggcgcgaga 3395
KEYWORDS
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3396 tggcgcctggagaagactggcggcctcggcgacgtcctcggggggcctccccgccgccA 532
3396 tggcgcctggagaagactggcggcctraggcgacgtcctcggccGcCCCCccccGGCCA 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jab host="SOLR" site_1: ECOR1; Site_2: xhol; /note="Wector: lambdaZAP; Site_1: ECOR1; Site_2: xhol; /note="Wector: lambdaZAP; site_1: ECOR1; Site_2: xhole /note="Wector: lambdaZAP; site_1: 10. 15. 20. /note="Wector: lambdaZAP; site_1: 10. 15. 20. /note="wector: lambdaZAP; site_1: 10. 15. 20. /note="wector: lambdaZAP; site_1: lambdaZAP
                                                                                                                                                                                                                                                                                                     3456 tggccgtaagcttgcgcc 3473
                                                                                                                                                                                                                                                       533 TGGCCGCCAACGGTCACC 550
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(/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%; in milarity 89.7%; of conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence analysis see
http://www.genome.clemson.edu/projects/barley gooder
http://www.genome.clemson.edu/orders Also
http://www.genome.clemson.edu/orders for
this clone see http://www.genome.clemson.edu/orders
see Close Ty, wing R, kleinhofs A, wise resources
see Close Ty, wing R, kleinhofs A, wise resources
see Close Ty, wing R, kleinhofs A, wise resources for
see Close Ty, wing R, kleinhofs Newsletter 31:29-30,
see Close Ty, wing R, kleinhofs Newslet
                                                            638 bp mrNA linear EST 04-JAN-2001
638 bp mrNA linear (3.-15.DAP)
AL508959 Hordeum vulgare Barke developing caryopsis (3.-15.DAP)
Hordeum vulgare cDNA clone HY10E20V 5', mRNA sequence.
               AL508959.1 GI:12035462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 293.2; DB
pred: No. 3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 558;
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AUTHORS
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ORIGIN
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Matches 338;
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                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                     3456 tggccgtaagcttgcgcc 3473
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3216 gttttcagggcctgaggcccggaacccggcggatgcggctcggcatgaggactgtcg 3275
                                                                                                                                                                                                                                                                                                                                                                                                            335 gaqcgaqcgccqcccaaagcaagcaggaaaccgcaccgattcgaccggcggtgcctct 3335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GTTTTCAGGGCCTCAGGCCCGGAACCCAGCGGATGCGGCCCTTGGTATGAGGACTATCG 362
                                                                                                                                                                                                             3336 ccatggtggtgcgccacgggcagcggcgcatgaacctcgtgttcgtcggcgcgaga 3395
                                                                                                                                                                                                                                                                                                                                      3396 tggcgcctggagcaagactggcggcctcggcgacgtcctcggggggcctccccggcca 3455
                                                                                                                                                                479 cogramacaracacacacaca---acagantanacaragramacaraacacacacanan 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / AU _ NUSE _ AUJUM. BR-CMY; Site_1: ECORI; Site_2: note _ Nector: plasmid pBK-CMY; Site_1 adaptopsis (3.-15.DAP) / Note _ Nector: plasmid pBK-CMY; Barke', a high quality malting / Note; may barley warlety barke', a high quality and xhol of spring loning sites: ECORI (5'-end of cDNA) and xhol of cDNA). NOTE: Due to ECORI site is NOTE is 1 kb variety. Cond of cDNA). NOTE: Due to ECORI site is NOTE is 1 kb variety. The ECORI cases the ECORI site is NOTE is 1 kb by the kit, in ECORI adapter. Average insert size ends were by the self adapter sequences and sequence window by the self as the ECORI adapter. Because and sequence trimmed from the 5'-and 3'-end until a 50 bp window sequence trimmed from the 5'-and ambiguities. The maximum length was contains less than two ambiguities. The maximum length was set to 700 bp 90 g 93 t 1 others
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/db_xref="taxon:4513"
/clone="HY10E20V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="developing caryopsis (3.-15.DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              %; Score 291.6; DB
%; Pred. No. 5e-33;
%; O; Mismatches
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BE414303 LOCUS

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RESULT 6
                                                                                                                               3389 gccgagatggcgcctggagcaagactggcggcctcggcgacg 3431
                                                                                                            597 GCGGAGATGGCGCCCTGGAGCAAGACCGGCGGCGTCGGCGACG 639
                                                                                                                                                                                    3329 tgcctctccatggtggtgcgcgccacgggcagcggcggcatgaacctcgtgttcgtcggc 3388
                                                                                                                                                              537 TGCCTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCGGCATGAACCTCGTGTTCGTCGCGC 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
                                                                                                                                                                                                                                                                 3272 gtcggagcgacgccccaaag---caaagcaggaaaccgcaccgattcgaccggcgg 3328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                           Query Match
Best Local Similarity 7.5%; Sc
Matches 313; Conservative 0;
                                                                                                                                                                                                                                                                                                                                              3212 ccaggttttcaggggcctgaggccccggaacccggcggatgcggcatggggcatgaggact 3271
                                                                                                                                                                                                                                                                                                                                                                                                   3092 atcagtogagtogtotottgotgoaggtagocacacocotgogogogocatggoggototg 3151
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VERSION
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Centre for Pro-
Po Box 157, Lismor enservation Genetics, Southern Cross University
Tel: 61 2 6620 3409
Email: the 1622 2080
International Triticeae EST Cooperative (ITEC)
Location/Qualifiers
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Triticum aestivum
Eukaryota; Viridip!
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/ob_xref="#Wyuna"
/ob_xref="taxon:4565"
/clone="SCU008.004"
/clone_lib="IPEC SU Wheat Endosperm Library"
/tissue_type="endosperm"
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SCU008.C04.R990714 ITEC 639 bp mRNA linear EST 24-JUL-2000
BE414303 CDNA clone SCU008.C04, mRNA sequence.
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BASE CORIGIN ORIGIN Query Best Match Match 233322 293 3292 353 C 352 C 413 C2 413 C2 614				
BASE COUNT 133 a  Query Match Best Local Similarity Matches 324; Conserv F 315 Caggtagccacac 173 CAGGTACCACACC 317 CTCGGCACCGCACCGCAAACCCAAACCCACACG 318 CCCGGAACCCACACG 319 CCCCGGAACCCACACG 11111111111111111111111	FEATURES Source	REFERENCE AUTHORS TITLE TURNAL COMMENT	LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	AT.SOOT
/Organ /Organ /Oulti /Organ /O	Correctute for Pin W Corrensstr. 3, Plant Genetics and Crop Plant Email: michalekeipk-Gatersleben, Germany Seq primer: Tarimer for 5 ond. Location/Qualifiers	Ins	H & L	
/outivar="Barke" vulgare" /outivar="Barke" vulgare Barke developing caryopsis /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="Hy07Ploy" /clone="My07Ploy" /clone="My07Ploy" /clone="Hy07Ploy" /clone	eaters and Crop Pla Gatersleben, German tersleben.de, http: for 5'end.	gare 'Iridiplantae, Streptophyta, 'a, Magnoliophyta, Liliopsida to 700) 'Weschke, W., Pleissner, Kp. '2000) analysis in barley	AL508163 AL508163 Hordeum vulgare 700 bp mRNA linear ES AL508163 vulgare cDNA clone HY07p10V 5', mRNA sequence. 3287. GI:12034378	
rrke developing caryopsis  Site_1: EcoRI; Site_2: ping caryopsis (315.DAP)*  Site_1: EcoRI; Site_2: ping caryopsis (315.DAP)  cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.DAP) cloning caryopsis (315.D	Op Plant Research Bermany http://pgrc.ipk-gaterslebo	bryophyta; Poales; Poa	linear EST g Carropsis (3.mrna sequence.	
ap Sen.de		Tracheophyta; ceae; Pooldeae	04-JAN-200J	<b>D</b> →

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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gagcgagcgccgccccaaagcaaagcaggaaaccgcaccgattcgaccggcggtgcctct 3335
                                                                                                       gttttcagggcctgaggccccggaacccggcggatgcggcgctcggcatgaggactgtcg 3275
                                                                                                                                                                                      cgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgtccag 3215
                                                                             GTTTTCAGGGCCTCAGGCCCCGGAACCCAGCGGATGCGGCGCTTGGTATGAGGACTATCG
                                                                                                                                                              CGTCCCAGCTCGCCACCTCCGGCACCGTCCTCGGNGTCACCGACAGATTCCGGCGTCCAG
                                                                                                                                                                                                                                                                                                                                      298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A EST sequencing and analysis in barley Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.
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Hordeum vulgare cDNA clone HY10D16V 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Corrensstr.3, D-06466 Gatersleben, Germany
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Michalek W
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                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XhoI; mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 by window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               set
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contains less than two ambiguities. The maximum length was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Hordeum vulgare Barke developing caryopsis
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/clone="HY10D16V"
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/cultivar="Barke"
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184 c 151 g
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Pred. No. 3.1e-28;
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                                   3272 gtcggagcgagcgccgccca---aagcaaagcaggaaaccgcaccgattcgaccggcgg 3328
                                                                                                                                                                                  3212 ccaggttttcagggcctgaggccccggaacccggcggatgcggcgtcggcatgaggact 3271
                                                                                                                                                                                                                                                                                                                                          3152 gtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgt 3211
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314 GTCACGTCGCAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watch 6.6%;
Local Similarity 83.5%;
                                                                                                                                                   GCAGGTTTTCAGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCCGCTCGGCATGAGGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G. International Triticeae EST Cooperative (ITEC): production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centre for Plant Conservation Genetics, PO Box 127, Lismore NSW 2480 AUSTRALIA Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: tholton@scu.edu.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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/note="Vector: Bluescript II SK(-)"

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/clone_lib="ITEC SCU Wheat Endosperm Library"
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/cultivar="Wyuna"
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Pred. No. 1.1e-26; 
0; Mismatches 57; Indels
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                                                                                   3223 gggcctgaggccccggaaccccggcggatgcggcgctcggcatgaggactgtcggaagcgag 3282
                                                                                                                                                                                                     3163 gctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgtccaggttttca 3222
3283 cgccgcccaaagcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggt 3342
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                                                        61 GGGCCTCAGGCCCCGGAACCCAGCGGATGCGGCCCTTGGTATGAGGACTATCGGAGCAAG 120
                                                                                                                                                                                                                                                                                        Match 6.5%; Score 247; DB 9; Length 700; Local Similarity 89.4%; Pred. No. 1.5e-26;
                                                                                                                                                         cgccgagatggcgccctggagc-aagactggcggcctcggcgacgtcctcggggggcctcc 3446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute for Plant Genetics and Crop Plant Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST sequencing and analysis in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: /note="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: /note="Vector: plasmid from developing caryopsis (3.-15.DAP) xhoI, mRNA was made from developing caryopsis (3.-15.DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI
                                                                                                                                                                                                                                                                                                                                                                                                                          set to 700 bp"
1 229 c 218 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contains less than two ambiguities. The maximum length was
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/lab_host="XLOLR"
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3099 cagtcgtctcttgctgcaggtagccacaccctgcgc---gcgccatggcggctctggtca 3155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Ramsay, L., Machray, G., Marshall, D.F.M. and Waugh, R. Development of Barley Transcriptome Resources Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: rwaugh@scri.sari.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Invergowrie,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Triticeae;
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00 44 1382 562426
                                                             Conservative
                                                                                                                                                                                                                               grains (6 days post anthesis) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating
                                                                                                                                                                                                                                                                                          /note="Vector: pSpORT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into pSpORT1 perived from endosperm tissue dissected from developing
                                                                                                                                                                                            Gene Function) project."
1 160 c 131 g 63
                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4513"
/clone="EBed01_SQ002_J02"
/clone_lib="IGF Barley EBed01 library"
                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Endosperm"
/dev_stage="6 days post anthesis"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cultivar="Optic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .444
                                                                                     6.1%;
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                                                               0; Mismatches
                                                                                   Score 231.4; DB 10; pred. No. 3.1e-24;
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                                                                   21; Indels
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                                                                                                             Length 444;
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                                                                        6;
                                                                        Gaps
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3156 cgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgtccag 3215

151 CAGTCGTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCCATGGCGGCTCTGGCCA 210

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ORGANISM
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AW448811
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                                                                                                                                                                                                                                                                                    Matches 290;
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                        3327
                                                                                                                                                                                                                                  3211 tccaggttttcagggcctgaggccccggaacccggcggatgcggctcggcatgaggac 3270
                                                                                                                                                                             3152 gtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccga-cagattccggcg 3210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 TACCGGAGCGAGCGCCCCCGAAGCAACAAAGCCGGAAAGCCCCACCGCGGGACCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
99tgcctctccatggtggtgcgcgccacgggcagcggcggcatgaacctcgtgttcgt-c 3385
                                                            tgtcggagcgagcgccccaaag---caaagcaggaaaccgcaccg-attcgaccggc 3326
                                                                                                    GTCACGTCGCAGCTCCGGCACCGTCCTCGGCATTACCGACCAGGTTCCGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTTCAGGGCCTCAGGCCCCGGAACCCAGCGGATGCGGCGCTTGGTATGAGGACTATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9agcgagcgccgcccaaagcaaagcaggaaaccgcaccgattcgaccggcggtgcctct 3335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gttttcagggcctgaggcccggaacccggcggatgcggcgctcggcatgaggactgtcg 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Bryan Clarke Division of Plant Industry C.S.I.R.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPO Box 1600, Canberra, ACT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clarke, B.C., Hobbs, M. and Appels, R. Genes active in developing wheat endosperm Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: bryanc@pi.csiro.au.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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BRY_1487 BRY Triticum aestivum cDNA clone P51-2A, mRNA sequence.
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61 2 6246 5000
                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="p51-2A"
                                                                                                                                                                                                                                                                                                                                                                     /cell_type="endosperm"
170 c 160 g
                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="BRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      location/Qualifiers
                                                                                                                                                                                                                                                                                               5.8%;
86.6%;
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                                                                                                                                                                                                                                                                                            Score 220.6; DB 9; Pred. No. 1.1e-22;
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β Q

179

3368 atgaacctcgtgttcgtcggcgcgagatggcgccctggagcaagactggcggcctcggc 3427

ATGAACCTCGTGTTCGTCGGCGCCCGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTTGGC

cgcaccgattcgaccggcggtgcctctccatggtggt-gcgcccacgggcagcggcggc 336

ATGCGGCGCTTGGTATGAGGACTATCGGAGCAAGCGCCCCCGAAGCAAAGCCGGAAAG 121

Db Db

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                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                    Matches 251;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                   3189 gcgtcaccgacagattccggcgtccaggttttcagggcctgaggccccggaaacccggcgg 3248
3249 atgcggcgctcggcatgaggactgtcggagcgagcgcccccaaagcaaagcaaggaaac 3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 GGTGCCTCTCCATGGTGGTGCGCCCACGGGCAGCGCCGGCATGAACCTGTGTTTCGTCC 455
                                                                                                                                                                                           Local Similarity
                                                                         N
                                                                  GCGTNACCGACAGATTCCGGCGTCCAGGTTTTCAGGGCCCTCAGGCCCCGGAACCCAGCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGCCCAAATGGCGCCCTGGAACAAAAAACGGGG 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A. EST sequencing and analysis in barley Unpublished (2000) Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de Seq primer: T3 primer for 5'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute for Plant Genetics and Crop Plant Research Corrensstr. 3, D-06466 Gatersleben, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticeae; Hordeum.
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                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                contains less than two ambiguities. The maximum length was set to 700 bp"
144 c 159 g 72 t 7 others
                                                                                                                                                                                                                                                                                                                                                                       Nnote="Vector: plasmid pBK-CMV; Site_1: EcoRI; Site_2: XNoI; mRNA was made from developing caryopsis (3.-15 DAP) of spring barley variety 'Barke', a high quality malting variety. Cloning sites: EcoRI (5'-end of cDNA) and XhoI (3'-end of cDNA). NOTE: Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter. Average insert size is 1 kb sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="developing caryopsis (3.-15.DAP)"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Hordeum vulgare Barke developing caryopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="HY02P18T"
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                                                                                                                                                                                        5.6%;
87.8%;
                                                                                                                                                                0;
                                                                                                                                                             Score 210.2; DB 9;
Pred. No. 3.7e-21;
0; Mismatches 31;
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                                                                                                                                                                                                         Length 462;
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                                                                                                                                                                                                                                                                                                                                                                      3212 ccaggttttcagggcctgaggccccggaacccggcggatgcggcgctcggcatgaggact 3277
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3152 gtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgt 3211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                       3272 gtcggagcgagcgccgcccaaagcaaagcag 3303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 ACCGGAGCGAGCGCCCCCGAAGCAACAAAG 373
                                                                                                                                                                                                                                                                                                                                                                                                                             222 GTCACGTCGCAGCTCGCCACCTCCGGCACCGTCCTCGGCATGACCGACAGGTTCCGGCGT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                   GCAGGTTTTCAGGGTGTGAGGCCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACT 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW448845 375 bp mRNA linear EST 03-JAN-2
BRY_1622 BRY Triticum aestivum cDNA clone P59-1E, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Bryan Clarke
Division of Plant Industry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
                                                                                                         1885 bp mRNA linear EST 24-JUL-2001
HWM002.B02 ITEC HWM Barley Leaf Library Hordeum vulgare cDNA clone
HWM002.B02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPO Box 1600, Canberra, ACT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 4.7%; Score 178.4; DB 9; Length Similarity 90.1%; Pred. No. 1.6e-16; 91; Conservative 0; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bryanc@pi.csiro.au
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genes active in developing wheat endosperm
                                                               EST
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                         Hordeum vulgare
                                              barley.
                                                                                  BE420745.1 GI:9418588
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/db_xref="taxon:4565"
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302 ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                   182 tctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagtg 241
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                               482 agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
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                                                                                                  ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                            Anderson,O.A., Appeis,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
Contact: Herrmann RG
Botanisches Institut der LMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://wheat.pw.usda.gov/genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: herrmann@botanik.biologie.uni-muenchen.de
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/db_xref="taxon:4513"
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/dev_stage="14 day old"
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Pred. No. 5.8e-08;
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/note="Genoscope sequence ID : COAG208DH12SP1-end
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40 others

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                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                            Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Burneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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/clone="208P24"
/clone_lib="G"
                            /db_xref="taxon:99883"
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                             cttgcttagaaaactttagtattttgattgtgtttttagttttttatttcattttgtttctt 661
                                                                             ctgtatttttttcattttctttcttctggaagggtaacactaatgccactaattcatt 601
                                                                                                                                               ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
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Similarity 47.7%;
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Pred. No. 3e-07;
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
Query
Match Length DB
                                                                                                                                                                                                                                                                                : /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:*

: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*

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ABL32184	ABL32717	ABL34492	ABL32411	AAS61386	ABL32859	AAS45300	AAS46519	ABL33246	AAI94064	ABL32148	AAQ26404	AAQ26401	ABL32357	AAI94068	ABL32053	ABL34022	AAS45477	AAS46336	ABL32905	ABL34358	AA195036	ABL32972	AAS46608	AA195044	ABL32267	AAS46774	ABL33696	ABL32098	ABL34155	ABL32527	AAS46686	ABL33697	AAS45347	$\omega$	7
	immune syst	metasta	immun	qene re	immune syst	മ	r suppressor		neurobl	Human immune syste	le-bo	SstI fr		neurobl	immune sys	Human immune syste	a	resso	immune	-	neurob	┷-	r	neurob	μ.	r suppressor	immune	immune syst	immune syst	immune	r suppressor	immune syst	ically pretre	immune svs	Tumour suppressor

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## ALIGNMENTS

RESULT
AAV29752
ID AAV2
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AC AAV2
XX
DT 11-S

AAV29752 standard; DNA; 4800 BP

AAV29752;

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misc_feature	misc_feature	repeat_region	repeat_region	repeat_region	Key repeat_region	Zea mays.	SER; starch-encapsulating glucosyl transferase; ss.	Zea mays waxy gene.	11-SEP-1998 (first entry)
/*tag= e /note= "GC stretch, potential regulatory factor binding" $442468$	/note= "direct repeat 1" /note= "direct repeat 1" 372385	/note= "direct repeat 1" 298302	/note= "direct repeat 1" 293.297 /*tage C	/note= "direct repeat 1" 288292 /*tag= b	Location/Qualifiers 283287 /*tag= a		SER; starch-encapsulating region; fusion vector; glucosyl transferase; ss.	ene.	irst entry)

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182.2 182.2 137.8 124.4 118.8 106.8 106.8

3.1.8 3.3.6 2.8 2.8 2.8 3.1

4800 2286 2542 1915 1915 2267 2267 6644 7372 7797 7996

AAV29752 AAQ45913 AAV29753 AAX60319 AAX633585 AAX33181 AAX33182 AAX33180 AAX33184

Oryza sativa waxy
DNA sequence of th
Granule bound star
Base sequence of t
Base sequence of t
Cowpox virus bsr f
Base sequence of t

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Description

Zea mays waxy gene Rice starch syntha

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821..828
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2761..2857
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/number= 2
1554..1684
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/number= 1
1220..1553
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1081..1219
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887..900
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2413..2513
/*tag= aa
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/number= 6
2290..2412
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/*tag= x
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2055..2144
/*tag= w
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/number= 2
1685..1765
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2651..2760
/*tag= cc
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/*tag= t
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/note= "transcriptional
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/note= "target duplication site (Ac7)"
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   exon
The sequence is that of the waxy gene which codes for glucosyl transferase. It can be used in the production of a hybrid polypeptide comprising a starch-encapsulating region (SER) fused to a payload protein. The hybrid polypeptide can be used to make modified starches comprising the payload protein, selected from, e.g. hormones, growth factors, antibodies, enzymes, dyes,
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                                                                                  Hybrid polypeptide comprising starch-encapsulating region and protein - useful for, e.g. producing protein(s) resistant to degradation by stomach acids
                                                                                                                          WPI; 1998-240100/21.
P-PSDB; AAW56484.
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                                                                   Example 2; Page 29-31; 156pp; English
                                                                                                                                                                        (EXSE-)
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                                                                                                                                                                                                             30-SEP-1997;
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/number= 10
3358..3489
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3102..3211
/*tag= ff
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3570..3572
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3395..3489
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4570..4575
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4593..4598
/*tag= ss
4597..4602
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3793..3879
**tag= mm
/number= 12
3880..3976
/*tag= nn
/number= 12
3977..4105
/*tag= oo
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/number= 13
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4106..4226
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/note= "target
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AC AAQ4
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DT 10-E
XX
DE Rice
XX
KW Amyl
KW anti
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Best_Local Similarity
Matches 415; Conserv
anti-sense;
                                     Rice starch synthase gene
                                                                    10-DEC-1993
                                                                                                                        AAQ45913 standard;
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              Amylose; gramineae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulins, etc. The modified starch can also be used to provide grain feeds enriched in amino acids. By encapsulating the payload protein in starch, it is more resistant to degradation by stomach acids.
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                                                                 (first entry)
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                                                                                                                        DNA; 2286
           modification; rice starch
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Pred. No. 6.2e-32;
0; Mismatches 235;
                                                                                                                        ВР
           synthase;
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Best Local Similarity
Matches 449; Conserv
         1321
                                                       3196
                                                                                                                                                 3136
                                                                                                                                                                                                                                                                                                                                                Rice starch synthase gene is used to transduce rice plants when ligated into a vector. This results in the amylose content of transduced plant being modified, improving the taste of the rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plant of rice family (family gramineae) with improved amylose content - in which vector is prepd. by transducing sense or anti-sense DNA of rice starch synthase gene downstream from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
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                                                                                                                                                                                                                                                                                                              Sequence 2286
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P-PSDB; AAR39441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 9-11;
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(MITU ) MITSUBISHI KASEI CORP
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                                                                                           caccatgtcggctctcaccacgtcccagctcgccacctcggccaccggcttcggcatcgc 1320
                                                                                                                    cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac
                                                  cgacagat---
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2100..2189
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1905
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/number= 3
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1604.1716
/*tag= c
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1798.1904
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/product= rice_starch_synthase
/note= "Stop codon not specified in specification."
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1265..2197
                                                                                                                                                                                                                                                                                                         578 A; 508 C;
                                                                                                                                                                                                           4.8%;
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                             -tccggcgtccaggttttcagggcctgaggccccggaa 3240
                                                                                                                                                                                            0;
                                                                                                                                                                                       Score 182.2; DB 14; Length 2286; Pred. No. 1.9e-31; O; Mismatches 198; Indels 78;
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AAV29753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER; starch-encapsulating region; fusion vector; starch synthase; bacterial glycogen; ss.
                                                                                                                                                                                                                                                                                  Oryza sativa waxy gene.
                                                                                                                                                                                                                                                                                                                 11-SEP-1998
                                                                                                                                                                                                                                                                                                                                                AAV29753;
                                                                                                                                                                                                                                                                                                                                                                            AAV29753 standard; DNA; 2542 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1978 tcgac 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3781 tcgac 3785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1918 acaggtacgagagggtgaggtttttccattgctacaagcgtggagtcgaccgtgtgttca 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3721 acaggtacgaggggtgaggtacttccactgctacaagcgcgggggtggaccgcgtgttcg 3780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1858 atttcgcaagattttaacccaagtttttgtggtgcaattcattgcagatcaaggttgcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3661 ctcctgcacatttctgcaagactttactgactggctggatctcgcagatcaaggtcgttg 3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1738 gtgatctctcctcggtacgaccagtacaaggacgcttgggataccagcgttgtggctgag 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3564 gtcatctccccgcgctacgaccagtacaaggacgcctgggacacccagcgtcatctccgag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3510 cctgccgttacaacgggtgccgt-----gtccgtgcaggccaacgggtcacgggtcatg 3563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3415 tggcggcctcggcgacgtcctcggggggcctccccgccgccatggccgtaagc----- 3466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1501 ---cggcgccggcatgaacgtcgtgttcgtcggcgcgagatggccccctggagcaagac 1557
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30-SEP-1997;
                               09-APR-1998
                                                                                                          polyA_site
                                                          W09814601-A1
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                                                                                                                                                                                                                                                                                                                 (first entry)
97WO-US17555
                                                                                                        /product= starch (bacterial glycogen) synthase
2535
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                                                                                                                                                                                                                           RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3196
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                                                                                                                                                                                                                                                                                               3415 tggcggcctcggcgacgtcctcgggggcctccccggccgccatggccg 3461
                                                                                                                                                                                                                                                                                                                                                                                                                                            3295 gcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccac 3354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3136 cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2542 BP; 610 A; 665 C; 693 G; 574 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       degradation by stomach acids
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                                                                                                                                                        AAX60319;
                                                                                                                                                                                          AAX60319 standard; DNA; 1915 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence of the maize waxy gene
                                                                                                                                                                                                                                                                             746 cggcggcctcggtgacgtcctcggtggcctcccccctgccatggctg 792
                                                                                                                                                                                                                                                                                                                                                 689 ---cggcgccggcatgaacgtcgtgttcgtcggcgccgagatggccccctggagcaagac 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 caccatgtcggctctcaccacgtcccagctcgccacctcggccaccggcttcggcatcgc 508
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                                                                                                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Pred. No. 2.7e-21;
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Non-glycogen-like polysaccharide production; fermentation; waxy gene; starch synthesis enzyme; glycogen-synthesis enzyme; glycogen synthesis;

non-starch branching gene; amylopectin; amylose; plant-like starch;

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Best Local :
                                   3440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes a method for the production of non-glycogen-like polysaccharides in a host. The method comprises transforming a host, suitable for fermentation, with genes encoding starch- or glycogen-synthesis enzymes, and fermenting the transformants. The specification also describes hosts transformed with a gene active in glycogen synthesis and at least one non-starch branching gene, involved in production of amylopectin or amylose in its original host. The method is used to produce plant-like starches by fermentation and new starches in plants. These starches are useful for all food and non-food applications of starch. The present sequence is used in
                                                                                                                                                                                                                              3260
                                                                                                                                                                                                                                                                                                                                                        3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1915 BP; 365 A; 610 C; 641 G; 299 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 49; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing non-glycogen-like polysaccharides in bacteria, fungi or plants - transformed with genes for enzymes involved in starch or glycogen synthesis allows fermentative production of starches with engineered properties
      301
                                                                  241
                                                                                                                                                                                              121
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                                                                                                                                  181
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                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                              1 atggcggctctggccacgtcgcagctcgtcgcaacgcgcgccggcctgggcgtcccggac 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               course of the invention.
                99cctccccgccatggccgtaagcttgcgcc 3473
                                                                                                                                                                                                                                                gcgtccacgttccgccgcggcgccgcgcagggcctgagggggcccggggcgtcggcggcg 120
                                                                                                                                                                                                                                                                              agattccggcgtccaggttttcagggcctgaggcccgggaacccggcggatgcggctc 3259
                                                                                                                                                                                                                                                                                                                                  atggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgac
ggcctgccgccggccatggccgcgaacgggcacc
                                                                            ttcgtcggcgccgagatggcgccctggagcaagactggcggcctcggcgacgtcctcggg 3439
                                                                                                                      cgccgcgggggcaggttcccgtcgtcgtcgtgtgcgccagcgccggcatgaacgtcgtc 240
                                                                                                                                          ttcgtcggcgcgagatggcgcgtggagcaagaccggcggcctcggcgacgtcctcggc
                                                                                                                                                                                  gcggacacgctcagcatgcggaccagcgcgcgcgcgcgcccaggcaccagcagcaggcg 180
                                                                                                                                                                                                                  1998-568285/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keeling PL;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97US-0042939
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                                                                                                                                                                                                                                                                                                                                                                                                3.3%;
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                              Score 124.4; DB Pred. No. 2.8e-18
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 1915;
                                                                                                                                                                                                                                                                                                                                                                                 0;
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AAX63355

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AAX63355 standard; cDNA;

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AAX63355

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                               3196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes an enzymatic nucleic acid molecule (I) with RNA cleaving activity, which modulates the expression of a plant gene. Also described is a gene comprising a cDNA sequence encoding maize belta-9 desaturase. (I) can be used to modulate expression of a gene, preferably Delta-9 desaturase or a granule bound starch synthase (GBSS) gene, in a plant (preferably a maize or canola plant). (I) can be used to modulate caffeine synthesis in a coffee plant, nicotine production in a tobacco plant, fruit ripening processes in an apple, tomato, pear, plum or peach plant, flower pigmentation in a rose, petunia, hearth and the processes in a pose of the pear, petunia, pear, pea
                                                                                                                                                         3304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2267 BP; 465 A; 699 C; 733 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chrysanthemum or marigold plant or lignin production in a aspen, poplar or pine plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       synthase in maize or canola
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribozyme which modulates plant gene expression -modulates expression of DELTA-9 desaturase or g_{\rm TZ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 9; Page 31-33; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-202224/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           granule bound starch synthase; hammerhead ribozyme; hairpin ribozyme; modulation; gene expression; transgenic plant; cleavage; canola plant caffeine synthesis; coffee plant; nicotine production; tobacco;
                 413
                                                                                                                                                                                                         293
                                                                                                                                                                                                                                                                                 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9710328-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fruit ripening; flower pigmentation; lignin production; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Granule bound starch synthase encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOWC ) DOWELANCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
cggcatgaacgtcgtcttcgtcggcgccgagatggcgccgtggagcaagaccggcggcct
                        cggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagcaagactggcggcct
                                                                                                                            gaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcgg
                                                                                                                                                                                                                     cggcatggcgctctagccacgtcgcagctcgtcgcaacgcgcgccggcctgggcgtccc 232
                                                                                                                                                                                                                                                                                                                                                                                                          cgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctcagcgtcac 3195
                                                                                              gcagcagcagccgcgcgcggggccaggttcccgtcgctcgtgtgcgccagcgc
                                                                                                                                                                                            cga----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIBOZYME PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Skokut TA,
                                                                                                                                                                                                                                                                                                                        -cagattccggcgtccaggttttcagggcctgaggccccggaacccggcgga 3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Folkerts 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0001135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US11689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O, Guo L,
Young SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118.8; DE 
Pred. No. 5.7e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McSwiggen
Zwick MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     granule
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tobacco,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
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                                                                                                                                                                             cell line into which an apoptosis resistance gene has been introduced.

CC associated genes. These can then be used in a variety of diseases for cwhich the induction of apoptosis by gene transfer, or where the cc inhibition of harmful apoptosis, is therapeutic. The recombinant viruses can then be used in a variety of diseases for cc which the induction of apoptosis by gene transfer, or where the cc inhibition of harmful apoptosis, is therapeutic. The recombinant viruses care useful as vectors for gene therapy which can be applied to cancer cc therapy for destroying cancer cells selectively, the treatment of cc autoimmune diseases and graff rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of the cells producing the virus will be destroyed because the period of cc time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated cc gene. In this invention an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-ires-bsr, which contains the cowpox virus bsr gene, and cc is used in an example from the present invention.
            δÃ
                                                   Matches 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; autoimmune disease; graft rejection reaction; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Base sequence of the plasmid pRx-ires-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX33181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX33181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 38-41; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hamada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (RPRG-) RPR GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1998;
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                                                                                                                                     Sequence 6644 BP; 2166 A; 1573 C; 1424 G; 1481 T; 0 other;
                                                                 Local
2 tttggtttcgctgtttttcatttccttcttaaggggtaataccaatgacagtaatt 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1999-243728/20
                                                                     Similarity
                                                                                                                                                                        in an example from the present invention.
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                                                     Conservative
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                                                                     2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS.
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                                                   0;
                                                                     Score 106.8; DB 20; Pred. No. 5.3e-14;
                                                     Mismatches 367;
                                                                 .3e-14;
                                                        Indels
                                                                                    Length
                                                                                           6644;
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                                                        0,
                                                        Gaps
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AAX33182/c
ID AAX331
XX
AC AAX331
AC AAX331
AC Base s
DE Base s
XX
Cowpox
KW Cowpox
KW CrmA,
KW autoin
KW inflan
XX
Synthe
OS Homo s
XX
PN W09913
XX
PN W09913
XX
PN 08-SEE
PF 07-SEE
XX
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                                                                                                                              crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; IIP; adenovirus; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4045
                                                                                                                                                                                                                                                                                                                                                        3805
                                                                                                                                                      Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
                                                                                                                                                                                                                                                       AAX33182 standard;
                                                                                                                                                                                                                                                                                                             3745 TTTTTTGCAACTGCAAGAGGGTTTATTGGATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
                                                                                                             Synthetic.
                                                                                                                                                                                     Base sequence of the plasmid pRx-Bcl-xl-bsr.
                                                                                                                                                                                                            25-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  302
                                                                           W09913073-A2
            08-SEP-1997;
                                  07-SEP-1998;
                                                       18-MAR-1999
                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtttcatgttttatttcattttctttacttttagggtaaaaccaatgcccccaattcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      catattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgttt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         totacotaagaggaaattoagttttatactagttttoagttttattattgtttattaagtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ctttaagggaaataccaatgccactaatccattc 695
                                                                                                                                                                                                                                                                                                                                                                    cttgcttagaaaactttagtattttgattgtgtttttagtttttatttcattttgtttctt 661
                                                                                                                                                                                                                                                                                                                                                                                                  ctgtatttttttttcatttttctttcttctggaagggtaacactaatgccactaattcatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                            agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                                                                                                                                                                                                                      (first entry)
             97JP-0259235
                                  98WO-JP04010
                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                         7372
                                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                             601
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C The recombinant viruses generated are capable of expressing apoptosis. CC associated genes. These can then be used in a variety of diseases for CC which the induction of apoptosis by gene transfer, or where the CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses CC are useful as vectors for gene therapy which can be applied to cancer CC therapy for destroying cancer cells selectively, the treatment of CC autoimmune diseases and graft rejection reaction, and apoptosis induction CC therapy for inflammatory cells in inflammatory diseases. Prior arts have CC encountered the problem where if an ademovirus vector capable of CC the required to induce cell death by apoptosis is shorter than that CC expressing an apoptosis-associated gene is introduced into animal cells, CC the cells producing the virus will be destroyed because the period of CC the required to induce cell death by apoptosis is shorter than that CC cobtain a recombinant virus having the integrated apoptosis-associated GC gene. In this invention an apoptosis-resistant 293 cell line (having an CC apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the CC plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and colored is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                             4893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7372 BP; 2353 A; 1749 C; 1649 G; 1621 T; 0 other;
482 agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 gtttcatgttttatttcattttctttactttttagggtaaaaccaatgcccccaattcat 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Page 41-45; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 catattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgttt 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 tttggtttcgctgtttttcatttcctttcttcttaaggggtaataccaatgacagtaatt 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                    ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag 361
                                                                                                                                                                                                                                                                                                                                                 ggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgct 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagtg 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%;
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Pred. No. 5.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Sequence 7797 BP; 2542 A; 1760 C; 1656 G; 1839 T; 0 other;

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CC The present invention describes an apoptosis-resistant virus-sensitive CC cell line into which an apoptosis resistance gene has been introduced. CT The recombinant viruses generated are capable of expressing apoptosis-CC associated genes. These can then be used in a variety of diseases for CC which the induction of apoptosis by gene transfer, or where the CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses CC are useful as vectors for gene therapy which can be applied to cancer CC therapy for destroying cancer cells selectively, the treatment of CC autoimmune diseases and graft rejection reaction, and apoptosis induction CC therapy for inflammatory cells in inflammatory diseases. Prior arts have CC encountered the problem where if an adenovirus vector capable of CC expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of CC time required to induce cell death by apoptosis is shorter than that CC contain a recombinant virus having the integrated apoptosis-associated CC gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the CC problem. The present sequence represents the cowpox virus bar gene which CC is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γQ
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AAX33180/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 34-38; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hamada H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New apoptosis-resistant virus-sensitive cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cowpox virus bsr full length gene sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4473 TTTTTTTGCAACTGCAAGAGGGTTTATTGGATAC 4440
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RESULT 9
AAX33184/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      5018
                                                          crmA; bc1-2; bc1-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer;
autoimmune disease; graft rejection reaction; inflammation;
                                                                                Cowpox virus; bsr; viral vector; expression; apoptosis; resistance;
                                                                                                  Base sequence of the plasmid pRx-Bcl 2-i-hCD
                                                                                                                          25-JUN-1999
                                                                                                                                                                  AAX33184 standard; DNA; 7996 BP
                                                                                                                                                                                                                                                                                                                                                                                                           422
                  Homo sapiens
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                                                 inflammatory disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    362
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                                                                                                                                                                                                                     TTTTTTTGCAACTGCAAGAGGGTTTATTGGATAC
                                                                                                                                                                                                                                        ctttaagggaaataccaatgccactaatccattc 695
                                                                                                                                                                                                                                                               agtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcatt 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                327;
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                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%;
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                                                                                                      25
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                                                                                                                                                                                                                                                                                    661
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cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of
                                     expressing an approtosis associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-Bcl 2-i-hcD 25, which contains the human Bcl-2 gene, and is used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 46-49; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-1997;
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Sequence 7996 BP; 2463 A; 2015 C; 1829 G; 1689 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97JP-0259235
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Matches 327
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                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                       totacctaagaggaaattoagttttatactagtttcagttttattattgtttattaagtg 241
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                                                                       gtttcatgttttatttcattttctttacttttagggtaaaaccaatgccccaattcat 181
                                    Conservative
                                                                                                                                                                                                                                                                      2.8%;
47.1%;
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Pred. No. 5.8
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           bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an
                                                                                                                                                                                                                                                                                                                                                     06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                            Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                                         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
                                                                                                                                                        Claim 1; SEQ ID No 459;
                                                                                                                                                                                                                                                       WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS46735 standard; DNA; 6292
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                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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  analysing
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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diseases associated with CpG dinucleotides
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                                                                                                                                                   27pp; English.
                                                                                                                                                                                                                                                                                 Berlin
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 e.g.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6292 BP; 1736 A; 99 C; 1304 G; 3153 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ttp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                              362
                                                                                                                                                                                                                                                                                                                                                                                                                    302
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                           ctttaagggaaataccaatgccactaatccattccatcttagaaaatctctttatcttac
                                                                                                                                  ctgtatttttttcatttttctttcttctggaagggtaacactaatgccactaattcatt
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                                                                                                                                                                                                                                                                                                                                                         ttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttcag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part printed specification, but was obtained in electron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 104; DB 22; Pred. No. 2.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL33958 standard; DNA; 14006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immune system associated
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                                                                               1906
                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofib
                                                                                                                                                                                                                                                                                                                     Claim
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for diagnosis and treatment
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002
                                                                                                                                                                                                                          rheumatoid arthritis,
                                                                                                                                                                                                                                                          including eye diseases such as retinopathy, neovascular glaucoma and
           202
                                                                                                       82
                                                                                                                                                                                                                                                                     present invention provides a number of human immune system associated es which are modified by the methylation of cytosines. The sequences be used in the diagnosis and treatment of immune system disorders,
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                                                                                               gttttatactagtttcagttttattattgtttattaagtgtttttagttggttttctcat 261
                               immune system disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                                                                                                                                          Similarity
                                                                                                                                                                                        14006 BP;
                                                                                                                                                                                                                                                                                                                                           methylation
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                                                                                                                              Conservative
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2000DE-1043826
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                                                                                                                                                                                                           zheimer's disease, AIDS, epilepsy, neurofibromatosis, thritis, psoriasis and inflammatory/ulcerative bowel present sequence is a gene of the invention.
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psoriasis; bowel dis
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                          human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                           Chemically pretreated complementary DNA associated with cell cycle #26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2386
                                                                                                                                                                                                                                                                                                                 Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; human immunodeficiency virus; neurodegenerative disorder; solid
                                                                                                                                                                                                                                                                                                                                                                                                           AAS45347
                                                              WPI; 2001-602751/68.
                                                                                                    (EPIG-)
                                                                                                                                                                                      15-MAR-2001;
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                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                immunosuppressive; antitumour; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                 Piepenbrock
                                      primers and probes for analysing diseases associated with
                                                                                                                         2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                        2001WO-EP02945
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associated

cell

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cytosine methylation state e.g. arthritis, arteriosclerosis comprising fragments of c

chemically cancer, aging

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RESULT :
XAXEX
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                                                                       ABL33697;
                                                                                                                      ABL33697 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of the diagnosis and d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9539 BP; 2078 A; 121 C; 2281 G; 5059 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atgaatattaggggtgtgtgtgcgtgtgttaatatacacataagtattatacacccattt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tttcagttttattattgtttattaagtgtttttagttggttttctcatttatgtgtatgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disease, Lewy body disease, arthritis, solid tumours and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101.6; DE
Pred. No. 9.7e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22; Length 9539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Best Local
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                                                                                                                                                                                                   2867
                                                                                                                                                                                                                                                    macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6668 BP; 1329 A; 328 C; 1736 G; 3274 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                            404 tttattttcttctttaagggtaataccaatgatactaatttatgcctcatttggaaattt 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 1670; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                      104 titotiittgtaattgtitgtitoatgtiittatticoattittottitaottititagggiaaaa 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-130909/17.
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                                                                                                                                                                                                                      224 attattgtttattaagtgtttttagttggttttctcatttatgtgtatgcatgaatatta
                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1670
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 48.8%;
                                                           aaaattatgcaatttcagtacaaattgtgcgcaaactcttcttcattttttattttat 403
9999t9t9t9t9c9t9t9thaatatacacataagtattatacacccatttttgcagtcat
                                                                                                                                                                                         ccaatgcccccaattcattctacctaagaggaaattcagttttatactagtttcagtttt
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       DB 24;
                                                                                                                                                                                                                                                                                                                                                                                         288;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6668;
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         The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases or the predisposition to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-APR-2000;
07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor gene derived chemically modified sequence #409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation; ds.
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                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID No 409; 27pp; English.
                                                                                                                                                                                                                                                                                                                                             analysing diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                               Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-2001; 2001WO-EP02955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgtgtaagttttgtcattctgtattttttttcatttttcttcttcttcttggaagggtaacac 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
by analysing cytosine methylations. The parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
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ABL3

2569 ttttt 2573

ABL32527 standard; DNA; 7571 BP

26-MAR-2002 (first entry)

ABL32527;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7442 BP; 1655 A; 214 C; 1934 G; 3636 T; 3 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                  2389
                                                                                                                                                                                                                                                                                                                                                           121 tgtttcatgttttatttcattttctttactttttagggtaaaaccaatgcccccaattca 180
                                                                                                                                                                                                                                                                                                                                                                                             301 gttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttca 360
                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                             661 tcttt 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 tcatattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgtt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tttttttttttttttagagttgcgtttttttatttagtgttttttagattttttagat 2028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ttotacctaagaggaaattcagttttatactagtttcagttttattattgtttattaagt 240
                                                                                                                                                                                                                                                             gggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatgc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent did not form part
                                                   tottgottagaaaactttagtattttgattgtgtttttagtttttatttcattttgtttct 660
                                                                                              tttttttttagttttttattttttttttcgaattttatttttatttttatttttagatttttat 2508
                                                                                                                                                              totgtattittittcattttttttttttttttggaagggtaacactaatgccactaattcat 600
                                                                                                                                                                                             tagtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagttttgtcat 540
                                                                                                                                                                                                                                                                                              46.8%;

 Mismatches

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4.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 7442;
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Best Local S
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                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-130909/17.
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                                                                     301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
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01-SEP-2000; 2000DE-1043826.
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0; Mismatches 435;
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Search completed: July Job time: 17362 sec 2002, 14:11:05

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Perfect score:
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Maximum DB seq length: 200000000
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Maximum Match 100%
Listing first 45 summaries
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## ALIGNMENTS

BASE COUNT ORIGIN	FEATURES source	T.	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AX349063	RESULT 1
/organism="Triticum aestivum" /db_xref="taxon:4565" 945 a 980 c 899 g 961 t	Location/Qualifiers 13785	Patent: W0 0202785-A 1 10-JAN-2002; Aventis CropScience GmbH (DE)	Sprunck, S., Kluth, A., Becker, D., Luetticke, S. and Loerz, H.	1 (sites)	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Triticum aestivum .	bread wheat.	•	AX349063.1 GI:18615098	AX349063		AX349063 3785 bp DNA linear PAT 06-FFR-2002		

	ac 1020     AC 1020	961 acacaacacatgagcactcacgcgagcacatgcatacacctgtgcgcacacaca	Qy Db
	at 960    AT 960	901 gtcgcatttttcatctctcacgcatgggcatgcataccctacacatgcacacaca	Оу
	9t 900	841 aatgccactaattccattccgtgagcacgcaatatgcggaatgcctacgtatattagtg	Qy Db
	CC 840	781 aattgcgtgcaaactttatcattatttgtctaaattaatt	Qy Db
	ta 780    TA 780	721 caaaaactcaacttttatatgottattcgtgcatattataaaaagcacagtttctatc 	Qу
	ta 720    TA 720	661 totttaagggaaataccaatgccactaatccattccatottagaaaatctotttatot 	Qу
	CT 660	601 tottgettagaaaaetttagtattttgattgtgttttagtttttattteattttgttt 	Фр
	at 600    AT 600	541 totgtatttttttttcattttotttotttottggaagggtaacaotaatgccactaattc 	Оу
	1t 540     T 540	481 tagtacacacttattcttgtatattatggaaaagcgcaatttctgtgtaagtttttgtca 	Оу
	C 480	421 gggtaataccaatgatactaatttatgcctcatttggaaatttcgttttgaaaattatg 	Qy Db
	la 420  -  A 420	361 gtacaaattgtgcgcaaactcttcttcattttttatttttattttattttcttc	Оу
	2a 360 1 2A 360	301 gttaatatacacataagtattatacacccatttttgcagtcataaaattatgcaatttc	Qу
	T 300	241 gtttttagttggttttctcatttatgtgtatgcatgaatattaggggtgtgtgt	Db dd
	t 240    T 240	181 ttctacctaagaggaaattcagttttatactagtttcagttttattattgtttattaag 	QУ
	180    A 180	121 tgtttcatgttttatttcatttttttacttttagggtaaaaccaatgcccccaattc 	Qy Db
	t 120     120	61 tcatattgtgtaacagtgcgattcttgtgccaattatgtacaatttcttttgtaattgt 	Qу
	H-t 60	1 gtttggtttcgctgtttttcatttcctttctttaaggggtaataccaatgacagtaa 	Qy Db
0;	аp	ry Match 100.0%; Score 3785; DB 6; Lengt t Local Similarity 100.0%; Pred. No. 0; ches 3785; Conservative 0; Mismatches 0; Indel	Que Bes Mat

tgcg 2100       GCG 2100		204	Dt. Qy
gtg 204      GTG 204	11 totatgacatgtgagoccaacagatggotggoccacatgtcagtgatccaaaggcag 	198	Qy Db
gtg 1980       GTG 1980	1 ctccactcaacgtcgcctttcaggacgatgcttcggtgccttaagacacctacct	192	Qy Db
tca 1920       TCA 1920	1. cgctcggcacgcacgcacgcaggcagaaacaaacaaacaa	186 186	Db Qy
JCTC 1860	1 caggetgecageegeteegegtaceactagtetegtacgtgtgecactecact	180 180	Qy Db
rtgc 1800         	1 aaaggegegteggeeaggeaeggeegcetggaaaggegegeeggegaacegagaatg 	174 174	Db VQ
cgc 1740      CGC 1740	1 agaagatgcgtgcacggcggcggcggcaacggaagggggcgccgcgccgagcgca 	168 168	. Qy
aca 1680      ACA 1680	1 gcgttggacatcacagcaggaacacccaccggcagcccaccgggcggg	162 162	Qy Db
tgc 1620      TGC 1620	1 agcgagagcacacatggcccccagaactgaaagcgagggagcacacgagaagggggg 	156 156	Qy Db
9 9	1 aggaagcaatcccgggccatgcagcgccattgccacgccccagcgaaaagcgaaggc 	150 150	Оу
cag 1500     CAG 1500	1 agcaaaagagaaaaagaaggggcgaaaggtgatacgcccggccgtgtcgtcgtgctg 	144	Qy ДЪ
4 4	. acgcgccggtttggcagcacgtacgtgctagctgttcataccagagccgtacgtcaa 	1381 1381	Qy
ctc 1380     CTC 1380	. gatocgacaaagccagggcacgtacgtgtccatgttggcacgtgcgtg	1321 1321	Qy Db
ccc 1320      CCC 1320	. caccaceteacegtgagtgacageceacegtegegtaaaceacegeatttaegttte	1261 1261	Qy Db
gct 1260     	togtaggacgaaaacggtcatatatgtggcactggccttctagagactctccaagagg 	1201 1201	Оу
ytg 1200   - 	aggtgccacagactagtattttcaggcgactgggatatagccacggcctattgtttcg	1141 1141	Qy Db
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TT 1080	cgacacacgcacagccacatgcgtgcacttagaaagaaaaatagacacgtataca 	1021	Qу

ggcgtccaggttttcagggcctgaggccccggaa 32	cgtcctcagcgtcaccgacagattcc	3181	Qy
tcccagetcgccacetccggc	ccacaccotgcgcgcgccatggcgg 	3121	Дb
taacaatcagt           TAACAATCAGI	aattetggtttaetteaeteae 	0 0	ob Qy
aaattcaaatgtaaaatccagaaaa                AAATTCAAATGTAAAATCCAGAAAA	ctctggtcatgttaatttggatttc 	3001	ръ
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tcacgcaccaaggctttg               TCACGCACCAAGGCTTTG	CTAGCCGAGTTGGATCAAAC	2821	g dg 04
JCAGCATAATGCGCGCATAAAC <i>E</i> 	CCTAGGGTTAATTACGACTAG	2761 2761	db dy
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aaaaaaagatttaaaatcatgi 	gatttaaaatcatgtaaaaattaa 	2641 2641	y dd dy
9cgagcgtaagttgaggatct              CGAGCGTAAGTTGAGGATCT	gtctcttcctttttacttaaag                 GTCTCTTCCTTTTTACTTAAAG	58	Дb
atccatccaaatgccgccatgttg 	ggtcggttggtctagtagtagata                  GTCGGTTGGTCTAGTAGTAGATA	2521 2521	p Q
gatggatagatcgatttagttcgg 	gcccaç            GCCCAC	2461 2461	р В
atcas       ATCAS	cagaagaagaagaagaaga               CAGAAGAAGAAGCAGAAGAAGA	2401 2401	Qу
gctccgtccaggaagaagaagaag 	aatgcccggccggcgactgtgagtac 	2341 2341	DP QA
tctgccagtgaaga               TCTGCCAGTGAAGA	Cacacactacaaccaggagcct                    CACACACTACAACCAGGAGCCT	2281 2281	B 8
TTC	actcaccggagccacgcaccgt                 ACTCACCGGAGCCACGCACCGT	2221 2221	DP GA
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tccggccgcgtgcatgcatgcacgaggagcggag 	tgccgtcccgtctaggcgttcggtg 	10	Оy

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RESULT 2
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2 (bases 1 to 2805)

Murai, J., Taira, T. and Ohta, D.

Direct Submission

Submitted (10-Nov-1998) Jun Murai, Osaka Prefectur.

College of Agriculture; 1-1 Gakuen-cho, Sakai, Osa

Japan (E-mail: junki@demeter.plant.osakafu-u.ac.jp,

Tel:81-722-54-9409, Fax:81-722-54-9409)
                                                                                                                                            Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the three Waxy granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
                                                                                                                                                                                                                        starch synthase (GBSSI).
Triticum aestivum DNA.
Triticum aestivum
Elikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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AB019622.1 GI:4760579
                                                                                                                                                                                                              (sites)
/organism="Triticum aestivum"
/db_xref="taxon:4565"
                                      Location/Qualifiers
                          . 2805
                                                                         Osaka Prefecture University,
-cho, Sakai, Osaka 599-8531,
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cgagagggtgaggtacttccactgctacaagcgcgggggtggaccgcgtgttcgtcgac 3785
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7gene="waxy"

9oin(13. .333,416. .496,581. .679,789. .942,1068. .1168,

1268. .1621,1713. .1892,1988. .2179,2270. .2356,2455. .2583,
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/protein_id="BAA77350.1"
/db_xref="GI:4760580"
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61
                                                                                                                                       AGATTCCGGCGTCCAGGTTTTCAGGGCCTGAGGCCCCGGAACCCGGCGGATGCGGCGCTC 120
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Triticum turgidum subsp.
(GBSSI), complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-Coho, Sakai, Osaka 599-8531, Japan (E-mail: junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409)
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GEDVVFVCNDWHTGLLACYLKSNYQSNGIYRTAKVAFCTHNISYQGRFSFDDPAQLNL
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/protein_id="BAA88509.1"
/db_xref="GI:6624281"
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KVPLVAFIGRLEEOKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEEKFPT
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1256. .1609,1701. .1880,1976. .2167,2258. .2344,2443. .
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/db_xref="taxon:85692"
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starch synthase (GBSSI).
Triticum durum DNA.
Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                        Submitted (16-JUN 1999) Jun Murai, Osaka Prefecture University, College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409)
                                                                                                                                                                                                                                                            Murai, J., Taira, T. and Ohta, D.
Isolation and characterization of the four Waxy ger granule-bound starch synthase in tetraploid wheats Appl. Biol. Sci. (1999) In press
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Triticum durum waxy gene
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join(1. .321,404. .484,569. .(
join(1. .1809,1701. .1880,1976.
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/db_xref="taxon:4567"
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AF474373
Hordeum vulgare BAC 259I16,
AF474373
AF474373.1 GI:18652401
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KVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEEKFPI
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VEGKTGFHMGRLSVCONVEYBADVKKVTTTLKRAVKVGTPAYHEMVKNCMIQDLSWK
GPAKNWEDVLLELGVEGSEPGIVGEEIAPLALENVAAP"
569 a 810 c 820 9 582 t
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No. 1.6e-111;
                            sequence
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-JAN-2002) Department of Biological Sciences, Purdue University, West Lafayette, IN 47907, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang, Z., Busso, C.S., Kleinhofs, A., Devos, K.M., Ramakrishna, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ma, J., SanMiguel, P.J., Dubcovsky, J., Shiloff, B.A., Rostoks, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Comparative sequence analysis of Wx1 homologous regions in barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bennetzen, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jiang, Z., Busso, C.S., Kleinhofs, A., Devos, K.M., Ramakrishna, W. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 124050)
Ma.J., SanMiguel, P.J., Dubcovsky, J., Shiloff, B.A., Rostoks, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 maize, pearl millet, rice, sorghum and diploid wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 124050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             join(6912.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(6912. .6997,7144. .7232,7460. .
8287. .8367,8772. .8832,8944. .8975)
/gene="259116.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="putative leucine aminopeptidase"
<6912. .>8975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(<6912. .6997,7144. .7232,7460. .
8287. .8367,8772. .8832,8944. .>8975)
/gene="259116.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="BAC 259116"
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/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Merex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(10203. .10391,11938.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="259116.2a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="259I16.2a"
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                                                                                                                                                                                                                                                                !SGRSSAIVPLDRPLCFSSLLTAEICMAPFGLGRVHVVGQPLIQSHMGKNQKRKRKNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .>12408
                                                                                                                                                 .>16939
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                                                                                                                                                                                                                 .15852,16734. .>16939)
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58592. .5866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(57099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(64715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to mudrA-like transposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transposon="LTR-retrotransposon BARE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(37482. .46140)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transposon="LTR-retrotransposon BARE-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28545. .37482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to putative non-LTR retrotransposon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transposon="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20238. .20342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>APTMPRPPSSMRPSATQSRRGLEGDELHGARVRLRMRLSPFPLSVDTSTGLEFGGEAR</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(18744.
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                                                                                                                                                                                                                                                           72677. .72709
                                                                                                                                                                                                                                                                                                               .
ARAFDAAAWRLGRLRRQINFQDVHTLQQALDVAPPPRVNSAQDRADHTARQRRLLVAQ
EDERVMAEWRRRHPEDVAYEQGYWARRREEDTRRRREERLDRRRRKALASAHADIVNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="259116.4"
70375. .70971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
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/gene="259116.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transposon="MITE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=
join(72864. .73181,73270. .73350,73435. .73533,73660. .7
73950. .74050,74165. .74518,74611. .74790,74885. .75076
                                                                                                                                                                                                                                                                                                                                                                translation="MPPRRRSASGYRGVRERPNGGFYAEIRSGDLRLSLGTYDTAHEA/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="259I16.4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_unit=at/
                                                                                                  /product="granule-bound starch synthase"
                                                                                                                                                                                                                                rpt_unit=gaa
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       Matches 1106;
                                                      72142 CCACTCAACAACAACAACACTCACTCACTCACGAGTGCCCCGCGACTGTGAGCACGCGCG
2252 ccttgagtcccgtcactttcgcccgcccgccccacaccactacaaccaggagcctcgatct 2311
                                                                               gene
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                                                                                                                              GTTTCCTTGGAGTCCCGTCACTTCCGCCCGCCCGCCCCCTACCACACACTACAACCTCTG
                                                                                                                                                                                                                     GCATGCATACATGCACGAGGAGCGGAGCGGGGGTATTGGGGGAT-CGGGCACCACGGG
                                                                                                                                                                                                                                                                                            Conservative
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83418. .84091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="unknown"
/protein_id="aal77110.1"
/protein_id="aal77110.1"
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LATRVPLHSAARLGSCYTRDGNNAFSNNSRRWFSSNEKHLPPISDPEIETAFKDLMAA
SWNELPGSLYEEAKKEVSKATDDKAGQEALENVFRAAEACEEFSGVLYTLRMALDDLC
GLTGENVGPLEGYKSAYSAYSRYMTYLESFGPEEHYLRKKVETELGTKMIHLKMRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="hypothetical protein"
<91421. .>92153
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join(<91421. .9151
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79967...80040,80132...80247))
/gene="259116.6"
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79967..80040,80132..>80247))
/gence="259116.6"
/product="unknown"
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EGKTGFHMGRLSVDCNVVEPADVKKVATTLKRAVKVVGTPAYQEMVKNCMIQDLSWKG
PAKNWEDVLLELGVEGSEPGIVGEEIAPLAMENVAAP"
                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="259I16.7"
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/gene="259I16.6"
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/protein_id="AAL77109.1"
/db_xref="GI:18652407"
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Pred. No. 2.8e-96;
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CCTCGGCGGCCTCCCCCGGCCATGGCCGTAAGCTAGCATCACGACACCCAACCATT
                 | CCtcggggggcttccccgccgccatggccgtaagcttgcgccactgc-----cttcttat 3486
                                                                      CCTCGTGTTCGTCGGCGCCGAGATGGCGCCCTGGAGCAAGACCGGCGGCCTTGGCGATGT
                                                                                            cetegtgttegteggegeegagatggegeeetggageaagaetggeggeeteggegaegt 3432
                                                                                                                                                                                                                                            caccgacagattccggcgtccaggttttcagggcctgaggccccggaacccggcggatgc
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                                                                                                                                                                   ccgattcgaccggcggtgcctctccatggtggtgcgcgccacgggcagcggcggcgtgaa
                                                                                                                                                                                                                      GGCGCTTGGTATGAGGACTATCGGAGCAAGCGCCGCCCCGAAGCAAAGCCGGAAAGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-JUN-1988) Zohde W., Max Planck Institute, Erwin Baur Institut, D-5000 Koln 30, FRG 2 (bases 1 to 5153)
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Structural analysis of the waxy locus from Hordeum vulgare
Nucleic Acids Res. 16 (14B), 7185-7186 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVWAXYG 5153 bp DNA linear Barley DNA for waxy locus encoding starch synthase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 5153)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     to bp 4647
                                                                                                                                                                                                          /number=1
990. .154
                                                                                                         join(1590. .1907,1997. .2077,2162. .2260,2387. .2540,
2677. .2777,2884. .3237,3330. .3509,3604. .3795,3878. .3964,
4062. .4190,4267. .4383)
                                                                                                                                                                                                                                            <988
                                                                                                                                                                                                                                                                                                                                                       /organism="Hordeum vulgare"
/strain="Vogelsanger Gold"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                         /cell_line="Vogelsanger Gold 519/15"
/tissue_type="leaf"
/clone_lib="EMBL4"
                           /product="starch synthase"
/protein_id="CAA30755.1"
/db_xref="GI:295809"
/db_xref="SWISS-PROT:P09842"
                                                                                                                                                          /number=2
                                                                                                                                                                                            /number=:
                                                                                                                                                                                                                                                                                                                                         /map="chromosome :
                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
/translation="maalatsqlatsgtvlgvtdrfrrpgfqglrprnpadaalgmrt
Igasaapkqsrkahrgsrrclsvvvsatgsgmnlvfvgaemapwsktgglgdvlgglp
                                                                                           codon_start=1
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1572 CACCCTGTGCGCGCGCCATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACC

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PWFLEKVRGKTREKIYGPDAGTDYEDNQORFSLLCQAALEAPRILNLANNPYESGPYG
EDVYFVCNDWHTGLLACYLKSNYQSNGIYRTAKVAFCIHNISYGGRSSEDDFAQLHL
DRFKSSFDFIDGYDKFVEGRKINWRKAGILQADKVLTVSPYYAEELISGEARGCELDN
IMRLTGITGINGMDVSEWDFTKDKFLAVNYDITTALEAKALNKEALQAEVGLPVDRK
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PAKNMEDVLLELGVEGSEPGIVGEEIAPLAMENVAAP"
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3796. .387
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2387. .25
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1997. .20
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2677. .2777,2884. .3237,3330.
4062. .4190,4267. .4377)
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              of the A, B and D proyeurses

Genome (1999) In press

2 (bases 1 to 2893)

Yan,L., Bhave,M., Fairclough,R., Konic,C., Rahman,S.

Direct Submission

Submitted (02-DEC-1998) School of Life Sciences and victoria University of Technology, Werribee Campus,

WCMC, Melbourne, Victoria 8001, Australia
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AF110375.
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Aegilops tauschii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Aegilops.
1 (Dases I to 2893)
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Aegilops
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organism="Aegilops tauschii"
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                                                    PO Box 14428
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/protein_id="AAP06938.1"
/db_xref="granule-bound starch synthase wx-TtD protein"
/protein_id="AAP06938.1"
/db_xref="granule-bound starch synthase wx-TtD protein"
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/db_xref="taxon:37682"
join(<32. .352,443. .523,620. .718,823. .976,1128. .1228,
1370. .1723,1809. .1988,2071. .2262,2347. .2433,2532. .2660,
2777. .>2893)
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<32. .>2893
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88.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (wx-TmA) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yan, L., Bhave, M., Fairclough, R., Konic, C., Rahman, S. and Appels, R Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                 578
                                                                             RKVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFERLLKSVEEKFP
SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDT
IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW
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                        KGPAKNWEHVLLELGVEGSEPGIVGEEIAPLAMENVAAP"
834 c 831 g 591 t
                                                                                                                                                                                  YGEDVVFVCNDWHTGLLACYLKSNYQSNG<sup>™</sup>YRTAKVAFCIHNISYQGRFSFDDFAQLN
LPDRFKSSFDFIDGYDKPVEGRKINWMKAGILQADKYLTVSPYYAEELISGEARGCEL
                                                                                                                                                                                                                                                                                        /translation="MAALVTSQLATSGAVLGITDRFRRAGFQGVRPRSPADAALGMRT
VGASAAPKQQSRKAHRGTRRCLSVVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(32. .355,444. .524,613. .711,830. .983,1127. .1227,
1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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1309. .1662,1752. .1931,2013. .2204,2288. .2374,2474. .2602,
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                                                                                                                                                                                                                                            DHPCFLEKVRGKTKEKIYGPDAGTDYEDNQLRESLLCQAALEVPRILDLNNNPYFSGP
                                                                                                                                                                                                                                                                     LPPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIKVADEYERVRYFHCFKRGVDRVFV
                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF06936.1"
/db_xref="GI:6318538"
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join(<32. .355,444. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3289 cccaaag---caaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggt 3345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GAGCAAGACCGGCGGCCTCGGCGACGTCCTCGGGGGCCTCCCCCAGCCATGGCCGTAAG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GAGGCCCCGGAGCCCGGCGGATGCGGCGCTCGGCATGAGGACTGTCGGAGCAAGCGCGGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 TACAAC--GTGCTGTGTCTATGCAGGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 GCGCGCCACGGCAGCGCCGCGCATGAACCTCGTGTTCGTCGGCGCCGAGATGGCGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                              599 ACTGGATCTCGCAGATCAAGGTCGCCGACGAGTACGAGCGGGTGAGGTACTTCCACTGCT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CACCTCCGGCGCCCTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTTCAGGGCGT 120
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                    Murai
                                                         Spermatophyta; Magnoliophyta;
Pooideae; Triticeae; Triticum.
                                                                                                                   Triticum aestivum
                                                                                                                                       Triticum aestivum DNA.
                                                                                                                                                        starch synthase (GBSSI).
                                                                                                                                                                            AB019624.1 GI:4760583
                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Isolation and characterization of the three Waxy genes encoding the
                                         (sites)
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                    Taira, T. and Ohta, D.
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89.7%;
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REFERENCE

AUTHORS

Murai, J., Taira, T. and Ohta, D

(bases 1 to 2886)

granule-bound starch synthase in hexaploid wheat

234 (1), 71-79 (1999)

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3600 tgggacaccagcgtcatctccgaggta-----tatatccgccacatgaattatcacaa 3652
                                                                                                                                                                           3484 tataaatgt----ttcttcctgcaggccatgccgtgtccggttaccaacgggtgccgtgtccgtg 3539
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                                                CAGGCCAACGGCCACCGGGTCATGGTCATCTCCCCGCGCTACGACCAGTACAAGGACGCC
                                                                          caggccaacggtcaccgggtcatggtcattctccccgcgctacgaccagtacaaggacgc 3599
                                                                                                                                                  CATAATGTTCATCTTGCAGTTGCAGCCATGCCTGCCGTTACAACGGGTGGTGTCCGTG
                                                                                                                                                                                                                                              GACGTCCTCGGGGGCCTCCCCCCAGCCATGGCCGTAAGCTAGACAGCACCACTGTCTTCT
                                                                                                                                                                                                                                                                                  gacgtcctcggggggcctccccgccgccatggccgtaagct----tgcgccactgccttct 348:
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DDRFKSSFDDF LOGYDKRVEGRKINWMKAGILQADKVLTVSPYYAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDITTALEGKALNKEALQAEVCLPVDR
KVPLVAFIGRLEEDKGEDVMITAIFEILKEEDVQIVLLGTGKKKFERLLKSIEEKFPS
KVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLGMRYCTPCACASTGGLVDTI
VEGKTGFHMGRLSVDCNVVEPADVKKYVTTLKRAVKYVGTPAYHEMVKNCMIQDLSWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="starch synthase (GBSSI)"
/protein_id="BAA77352.1"
/protein_id="BAA77352.1"
/db_xref="GI:4760584"
/tanslation="MAALVTSCLATSGTVLGITDRERRAGFQGVRPRSPADAALGMRT
VGASAAPTOSRKAHRGTRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGGL
PPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIKVVDKYERVRYFHCYKRGVDRVFVD
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join(13. .333,424. .504,600. .698,803. .956,1109. .1209,
join(13. .3704,1790. .1969,2052. .2243,2328. .2414,2513. .2641,
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/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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Submitted (16-JUN-1999) Jun Murai, Osaka Prefecture University,
College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531,
Japan (E-mail:junki@demeter.plant.osakafu-u.ac.jp,
Tel:81-722-54-9409, Fax:81-722-54-9409)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triticum durum DNA.
Triticum turgidum subsp. durum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Appl. Biol. Sci. (1999) In pre 2 (bases 1 to 2804)
Murai, J., Taira, T. and Ohta, D.
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                       577
                                                                                                  /product="starch synthase (GBSSI)"
/product="starch synthase (GBSSI)"
/product="starch synthase (GBSSI)"
/product="starch synthase (GBSSI)"
/product="starch synthase (GBSSI)"
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HPCFLEKVRGKTKEKIYGPDAGTDYEDNQLRFSLLCQAALEAPRILDLNNNPYFSGPV
HPCFLEKVRGKTKEKIYGPDAGTDYENGYTMAKVAPCIHNLSYQGRFSFDDFAQLNL
GEDVVFVCNDWHTGLLACYLKSBYQSNGIYMTAKVAPCIHNLSYQGRFSFDDFAQLNL
PDRFKSSEDFIDGYDKFVGGRKINWKRAGILQADKVLTVSPYYAEELISGEARGCELD
NIMRLTGITGIVNGMDVSEWDPTKDKFLAVNYDVTTALEGKALNKEALQAEVGLPVDR
KYVPLVAFTGRLEEGKGDDVMIAAIPEILKEEDVGIVLLGTGKKKFERLLKSVEEKFPN
KYVPLVAFTGRLEEGKGDDVMIAAIPEILKEEDVGIVLLGTGKKFERLLKSVEEKFPN
KYVPLVAFTGRLEEGKGDDVMIAAIPEILKEEDVGIVLLGTGKKFERLLKSVEEKFPN
                                                          KVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDTI
VEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHGMVKNCMIQDLSWK
                                       GPAKNWEDVLLELGVEGSEPGVIGEEIAPLAMENVAAP"
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1293. .1646,1731. .1910,1993. .2184,2265. .2351,2439. .2567,
                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="waxy"
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1293. .1646,1731. .1910,1993. .2184,2265. .2351,2439.
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for starch synthase (GBSSI), complete cds.
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Best Local Similarity

13.1%;

Score 495.2; DB Pred. No. 3e-84;

8;

Length 2804;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gaccggcggtgcctctccatggtggtgcgcgcaccgggcagcggcatgaacctcgtg 3379
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                                                                                                                                                                                                                                                                                                                                                             tcgtcgac 3785
                                                                                                                                                                                                                                   AB019623 2818 bp DNA linear PLN 05-AL Triticum aestivum gene for starch synthase (GBSSI), complete AB019623
             Murai, J., Taira, T
Direct Submission
                                                                 Isolation and characterization of the three Waxy genes granule-bound starch synthase in hexaploid wheat Gene 234 (1), 71-79 (1999)
                                                                                                                                                                               Triticum aestivum
                                                                                                                                                                                              Triticum aestivum DNA.
                                                                                                                                                                                                         starch synthase (GBSSI).
                                                                                                                                                                                                                      AB019623.1 GI:4760581
                                                                                                           Murai, J., Taira, T. and Ohta, D.
                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Submitted (10-NOV-1998) Jun Murai, Osaka Prefecture University,
                                                        99321800
                                                                                                                                        Pooideae;
                                                                                                                                                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                        (bases 1 to 2818)
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                        Taira, T. and Ohta, D.
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                    3585 cagtacaaggacgcctgggacaccagcgtcatctccgaggt----atatatccgccacat 3640
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        478
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       CAGTACAAGGACGCCTGGGACACCAGCGTCGTCTCCGAGGTACACATATATCCGCCACAT
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3128 cctgcgcgccatggcggctctggtcacgtcccagctcgccacctccggcaccgtcctc 3187
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GATGCTGTGTC--TGCAGGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCGCTACGAC
                           ggtgccgtgtccgtgcaggccaacggtcaccgggtcatggtcatctccccgcgctacgac 3584
                                                                                                               GTCTTCTGAT-AATGTTTCTTCTTGCAGCCAGCCATGCCTGCCATTACAAGTTTACAACT 419
                                                                                                                                                                        gccttcttataaatgtttcttcctgcagccatgcctgcc---
                                                                                                                                                                                                                              College of Agriculture; 1-1 Gakuen-cho, Sakai, Osaka 599-8531, Japan (E-mail:)unki@demettr.plant.osakafu-u.ac.jp, Tel:81-722-54-9409, Fax:81-722-54-9409) [location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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TGASAPROGSIKAHRGITERCLISMYVKATGSAMILLYVGAEVARPOSTGGLODVIGG

LPPAMAANGHRVMYISPRYDQYKDAWDTSVVSEIKVADEYBEVYREIGYKRGVDRVEY

DHPCELEKVRGKKKEKTYGPDAGTDYEDNOLRESLLOQAALEAPRILDLINNPYFSGP

YGEDVVEVGINWHTGLLACYLKSNYOSSGIYERAKVAFCIHNISYGGREFSDDFAQLU

LPDRFKSSFDEIDGYDKPVEGRKINWHKAGILQADKVLTVSPYYAEBLISGEARGCEL

DNIHRLIGGITGIVNGMJYSEWDPAKDKTLAANVDVTTALEKSLINKEALQAEVGLEVD

RKVPLVAFIGRILEEOKGPDVMIAAIPEILKEBDVQIVLLGTGKKKEFELLKSVEEKFV

SKVRAVVERNAFLAHQMAGADVLAVTSRFEPCGLIOLQGMRYGTPCACASTGGLVDT

INEGKTGFHMGRLSVDCNYVERADVKKVTTLKRAVKVVGTPAYHEMVKNCMIODLSW
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/protein_id="BAA77351.1"
/db_xref="GI:4760582"
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join(13. .336,436. .516,605. .703,817. .970,1104. .12)
1274. .1627,1720. .1899,1986. .2177,2262. .2348,2446.
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1274. .1627,1720. .1899,1986. .2177,2282. .2348,2446. .2574,
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/db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-DEC-1998) School of Life Sciences and Technology, Victoria University of Technology, Werribee Campus, PO Box 14428 MCMC, Melbourne, Victoria 8001, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome (1999) In press 2 (bases 1 to 2826)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yan, L., Bhave, M., Fairclough, R., Konic, C., Rahman, S. and Appels, R. The genes encoding granule-bound starch synthases at the waxy loci of the A, B and D progenitors of common wheat
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Regilops speltoides

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Lilliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yan,L., Bhave,M., Fairclough,R., Konic,C., Rahman,S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aegilops speltoides granule-bound starch synthase WX-TsB protein (WX-TsB) gene, complete cds.
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                                                                     /product="granule-bound starch synthase wx-TsB protein"
/protein_id="AAR06937.1"
/db_xref="gr:6318540"
/translation="MAALVTSQLATSATVLGITDRERHAGFQGVRPRSPADAPLGMRT
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VGASAAPKQQSRKAHRGTRRCLSMVVRATGSGGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRVMVISBRYDQYKDAWDTSVVSEIKVADEYERVRYFHCYKRGVDRVFV
VGASAAPKQQSKKAHKGITGDXCDAWDTSVVSEIKVADEYERGP
LPPAMAANGHRVMVISBRYDQYKDAWDTSVVSEIKVADEYERGPILLNUNPYESGP
YGEDVVFVCNDWHTGLLACYLKSNYQSMGISTAKVAFCIHNISYQGRESFDDFAQLN
LPDREKSPEDFIDGYDKPVEGRKINWMKAGILGADKVLTVSPYYABELLISGEARGCEL
DNIMELTGITGITVNGMDVSEMDPTKDMFLAANUNITTALEGKALNKEALQAEVGLPVD
RKVPLVAFIGRLEGQKGPDVMIASIPEILKEEDVQIVLTGGKKKFERLLKSVEEKFP
SKVPANVDENNDEI ABOMMAGANUN AVMEDEEDDGGITGTGTGAMSGTGTTAN
                        SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLYDT
IVEGKTGFHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMVKNCMIQDLSW
KGPAKNMEDVLLELGVEGSEPGYIGEEIAPLAMENVAAP"
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join(32. .355
1316. .1669,1
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/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Aegilops speltoides"
/cultivar="AUS 21638"
/db_xref="taxon:4573"
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Murai,J., Taira,T. and Ohta,D.
Isolation and characterization of the four Waxy genes granule-bound starch synthase in tetraploid wheats
Appl. Biol. Sci. (1999) In press
2 (bases 1 to 2793)
                                                                                                                 Triticum turgidum subsp. dicoccoides (sub_species:dicoccoides) DNA. Triticum turgidum subsp. dicoccoides Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticum.
                                                                                                                                                                                                                                                                                                                       AB029062
Triticum turgidum subsp.
                                                                                                                                                                                                                                    starch synthase (GBSSI).
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                     3537 gtgcaggccaacggtcaccgggtcatggtcatctccccgcgctacgaccagtacaaggac 3596
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419 -TGCAGGCCAACGGTCACCGGGTCATGGTCATCTCCCCGCGCTACGACCAGTACAAGGAC 477
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                                                                                                 ATGTTTCTTCTTGCAGCCAGCCATGCCTGCCATTACAAGTTTACAACTGATGCTGTGTC- 418
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SKVRAVVRFNAPLAHQMMAGADVLAVTSRFEPCGLIQLQGMRYGTPCACASTGGLVDT
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YGBDYVFVCNDRIFGLLACYLKSNYQSSGIYSTAKAFCIHNISYQGRESFDDFAQLN
LPDRFKSSFDFIDGYDKFVEGRKINWKAGGILQADKVLTVSPYYABELISGEARGCEL
DNIMRLTGITGIVNGMDVSEMDPAKDKFLAANYDYTTALBGKALNKEALQAEVGLPVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="maalvTSQLATSGTVLGITDRFRRAGFQGVRPRSPADAPLGMRT
TGASAAPKQQSRKAHRGTRRCLSMVVKATGSAGMNLVFVGAEMAPWSKTGGLGDVLGG
LPPAMAANGHRVMVISPRYDQYKDAWDTSVVSEIKVADEYERVRYFYEYKRGVDRVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="starch synthase (GBSSI)"
/protein_id="BAA88510.1"
/db_xref="GI:6624283"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       join(1. .324,424. .504,593. .691,805. .958
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1262. .1615,1708. .1887,1974. .2165,2249. .2335,2433. .2561,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding the waxy protein Plant Mol. Biol. 16 (6), 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clark, J.R., Robertson, M. and Ainsworth, C.C. Nucleotide sequence of a wheat (Triticum aestivum L.) cDNA clone
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FSFDDFAQLNLPDRFKSSFDFIDGYDKPYEGRKINMKAGILQADKYLTVSPYYAEEL
ISGEARGCELDNIMRLTGITGIVNGMDVSEMDPIKDKFLTVNYDVTTALEGKALNKEA
                                         VGASAAPKOSRKPHREDRRCLSMVVRATGSGGMNLVFVGAEMAPPGKTGGLGDVLGGL
PAANAANGHRVMVLSPKYDQYKDAWDTSVLSELKVVDRYERVRYFHCYKRCDDRVFVD
HPOELEKVRGKTKEKTKGPDAGTDYBUDQQRFSLLCQAALEVPRLLDLNINHPISGPY
AMLCRAVPRRAGEDVVFVCNDWHTGLLACYLKSNYOSNGLYRTARVAFCHHLSYQGR
                                                                                                                                                                                        /product="glycogen (starch) synthase"
/protein_id="CAA40509.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="endosperm"
/clone_lib="lambda gt10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="pcSS22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="7A, 7B, 4B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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                                                                                                                           translation="MAALVTSQLATSGTVLSVTDRFRRPGFQGLRPRNPADAALGMRT/
                                                                                                                                                 /db_xref="SWISS-PROT:P27736"
                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                             /EC_number="2.4.1.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_line="Chinese spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
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                                                                                                                                                                                                AUTHORS
TITLE
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JOURNAL
MEDLINE
                                                                                                                                                                             JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                    gene
                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3452 gccatggccgtaagcttgcgccactgccttcttat 3486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3392 gagatggcgccctggagcaagactggcggcctcggcgacgtcctcggggggcctccccgcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3332 ctctccatggtggtgcgccacgggcagcggcggcatgaacctcgtgtttcgtcggcgcc 3391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCGGAGCGAGCGCCCCAAAGCAAAGCAGGAAACCGCACCGATTCGACCGGCGGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGTTTTCAGGGCCTGAGGCCCCGGAACCCCGGCGGATGCGGCGCTCGGCATGAGGACT 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ccaggttttcagggcctgaggcccggaacccggcggatgcggcgctcggcatgaggact 3271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9tcacgtcccagctcgccacctccggcaccgtcctcagcgtcaccgacagattccggcgt 3211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-DEC-1998) Crop Breeding, Tohoku National Experiment Station, Shimo-Kuriyagawa, Morioka, Twate 020-01, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF113844 2028 bp mRNA linear PLN 20 Triticum aestivum granule-bound starch synthase precursor mRNA, Wx-Dlb allele, complete cds.
                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                         Vrinten, P.L. and Nakamura, T.
                                                                                                                                                                                                                                                 Molecular characterization of waxy mutations Mol. Gen. Genet. 261 (3), 463-471 (1999) 99254805
                                                                                                                                                                                                                                                                                                Vrinten, P., Nakamura, T. and Yamamori, M.
                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

1 (bases 1 to 2028)
                                                                                                                                                                                                                                                                                                                                                                                       Triticum aestivum
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                                                                                                                                    Shimo-Kuriyagawa, Mc
Location/Qualifiers
mutated Wx-D1 gene"
             /note="Wx-Dlb null allele
                                                                   /db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIAREVGLPVDRKVPLVAFIGRLEEQKGPDVMIAAIPEIVKEEDVQIVLLGTGKKKFER
LLKSVEEKFPTKVRAVVRENAPLAHQMMAGADVLAVTSRFEPCGLIQLGGMRYGTPCA
CASTGGLVDTIVEGKTGEHMGRLSVDCNVVEPADVKKVVTTLKRAVKVVGTPAYHEMV
KNCMIQDLSWKGPAKNWEDVLLELGVEGSEPGIVGEEIAPLALENVAAP*
a 638 c 694 g 387 t
                                 /gene="Wx-D1"
                                                                                      /organism="Triticum aestivum"
/cultivar="Waxy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:4588608
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     of Waxy wheat; spontaneously
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
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                                                                                                                                                                      3291 caaagcaaagcaggaaaccgcaccgattcgaccggcggtgcctctccatggtggtgcgcg 3350
                                                                                                                                                                                                                                                                                                    3171
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 361
                                                       301
                                                                                                          241
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                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                     1 GCTGCAGGTAGCCACACCCTGCGCGCGCGCATGGCGGCTCTGGTCACGTCCCAGCTCGCCA 60
                                                              agactggcggcctcggcgacgtcctcgggggcctccccgccgccatggccgtaagcttgc 3470
                                                                                                                  ocacgggcagcggcatgaacctcgtgttcgtcggcgccgagatggcgccctggagca 3410
                                                                                                                                                                                                                             CCTCCGGCACCGTCCTCGGCATCACCGACAGGTTCCGGCGTGCAGGTTTCCAGGGCGTGA 120
                                                                                                                                                                                                                                                                              cotcoggcaccgtcctcagcgtcaccgacagattccggcgtccaggttttcagggcctga 3230
ACCGGGTCATGGTCAT 376
                         gccactgccttcttat 3486
                                               AGACCGGCGCCTCGGCGACGTCCTCGGGGGCCTCCCCCAGCCATGGCCGCCAACGGCC 360
                                                                                                  CCACCGCAGCGCCGCATGAACCTCGTGTTCGTCGGCGCGAGATGGCGCCCTGGAGCA
                                                                                                                                                                                                             GGCCCCGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGCCC 180
                                                                                                                                                          CAACGCAAAGCCGGAAAGCGCACCGCGGGGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG
                                                                                                                                                                                                                                                                                                                                                                                 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               448 a
                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPAWKVSR"
a 614 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="granule-bound starch synthase precursor"
/protein_id="AAD26156.1"
/db_xref="GI:4588609"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Waxy protein; non functional"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Wx-D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /allele="Wx-D1b"
30. .1754
                                                                                                                                                                                                                                                                                                                                                                                            8.3%;
                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                        Score 315.2; DB 8; Pred. No. 6.4e-50;
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